

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Choi et. al.
- (ii) TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
- (iii) NUMBER OF SEQUENCES: 454
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Human Genome Sciences, Inc.
  - (B) STREET: 9410 Key West Avenue
  - (C) CITY: Rockville
  - (D) STATE: Maryland
  - (E) COUNTRY: USA
  - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
  - (B) COMPUTER: Dell Latitude C610
  - (C) OPERATING SYSTEM: Windows 2000
  - (D) SOFTWARE: ASCII Text
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 09/765,272
  - (B) FILING DATE: January 22, 2001
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/961,083
  - (B) FILING DATE: OCT-30-1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Lin J. Hymel
  - (B) REGISTRATION NUMBER: 45,414
  - (C) REFERENCE/DOCKET NUMBER: PB340P2C2
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (301) 610-5790
  - (B) TELEFAX: (301) 309-8439

## (2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1999 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TAAAATCTAC GACAATAAAA ATCAACTCAT TGCTGACTTG GGTTCCTGAAC GCCGCGTCAA	60
TGCCCCAAGCT AATGATATTC CCACAGATTT GGTTAAGGCA ATCGTTTCTA TCGAAGACCA	120
TCGCTTCTTC GACCACAGGG GGATTGATAC CATCCGTATC CTGGGAGCTT TCTTGCGCAA	180
TCTGCAAAGC AATTCCCTCC AAGGTGGATC AACTCTCACC CAACAGTTGA TTAAGTTGAC	240
TTACTTTTCA ACTTCGACTT CCGACCAGAC TATTTCTCGT AAGGCTCAGG AAGCTTGGTT	300
AGCGATTGAG TTAGAACAAA AAGCAACCAA GCAAGAAATC TTGACCTACT ATATAAATAA	360
GGTCTACATG TCTAATGGGA ACTATGGAAT GCAGACAGCA GCTCAAACT ACTATGGTAA	420
AGACCTCAAT AATTTAAGTT TACCTCAGTT AGCCTTGCTG GCTGGAATGC CTCAGGCACC	480
AAACCAATAT GACCCCTATT CACATCCAGA AGCAGCCCAA GACCGCCGAA ACTTGGTCTT	540
ATCTGAAATG AAAAATCAAG GCTACATCTC TGCTGAACAG TATGAGAAAG CAGTCAATAC	600
ACCAATTACT GATGGACTAC AAAGTCTCAA ATCAGCAAGT AATTACCCTG CTTACATGGA	660
TAATTACCTC AAGGAAGTCA TCAATCAAGT TGAAGAAGAA ACAGGCTATA ACCTACTCAC	720
AACTGGGATG GATGTCTACA CAAATGTAGA CCAAGAAGCT CAAAAACATC TGTGGGATAT	780
TTACAATACA GACGAATACG TTGCCTATCC AGACGATGAA TTGCAAGTCG CTTCTACCAT	840
TGTTGATGTT TCTAACGGTA AAGTCATTGC CCAGCTAGGA GCACGCCATC AGTCAAGTAA	900
TGTTTCCTTC GGAATTAACC AAGCAGTAGA AACAAACCGC GACTGGGGAT CAACTATGAA	960
ACCGATCACA GACTATGCTC CTGCCTTGGA GTACGGTGTC TACGATTCAA CTGCTACTAT	1020
CGTTCACGAT GAGCCCTATA ACTACCCTGG GACAAATACT CCTGTTTATA ACTGGGATAG	1080
GGGCTACTTT GGCAACATCA CCTTGCAATA CGCCCTGCAA CAATCGCGAA ACGTCCCAGC	1140
CGTGGAACCT CTAAACAAGG TCGGACTCAA CCGCGCCAAG ACTTTCCTAA ATGGTCTAGG	1200
AATCGACTAC CCAAGTATTC ACTACTCAAA TGCCATTTCA AGTAACACAA CCGAATCAGA	1260
CAAAAAATAT GGAGCAAGTA GTGAAAAGAT GGCTGCTGCT TACGCTGCCT TTGCAAATGG	1320
TGGAACCTAC TATAAACCAA TGTATATCCA TAAAGTCGTC TTTAGTGATG GGAGTGAAAA	1380
AGAGTTCTCT AATGTCGGAA CTCGTGCCAT GAAGGAAACG ACAGCCTATA TGATGACCGA	1440
CATGATGAAA ACAGTCTTGA CTTATGGAAC TGGACGAAAT GCCTATCTTG CTTGGCTCCC	1500
TCAGGCTGGT AAAACAGGAA CCTCTAATA TACAGACGAG GAAATTGAAA ACCACATCAA	1560
GACCTCTCAA TTTGTAGCAC CTGATGAACT ATTTGCTGGC TATACGCGTA AATATTCAAT	1620
GGCTGTATGG ACAGGCTATT CTAACCGTCT GACACCACTT GTAGGCAATG GCCTTACGGT	1680
CGCTGCCAAA GTTTACCGCT CTATGATGAC CTACCTGTCT GAAGGAAGCA ATCCAGAAGA	1740
TTGGAATATA CCAGAGGGGC TCTACAGAAA TGGAGAATTC GTATTTAAAA ATGGTGCTCG	1800

TTCTACGTGG AACTCACCTG CTCCACAACA ACCCCCATCA ACTGAAAGTT CAAGCTCATC 1860  
 ATCAGATAGT TCAACTTCAC AGTCTAGCTC AACCCTCCA AGCACAAATA ATAGTACGAC 1920  
 TACCAATCCT AACAATAATA CGCAACAATC AAATACAACC CCTGATCAAC AAAATCAGAA 1980  
 TCCTCAACCA GCACAACCA 1999

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 666 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Ile Tyr Asp Asn Lys Asn Gln Leu Ile Ala Asp Leu Gly Ser Glu  
 1 5 10 15  
 Arg Arg Val Asn Ala Gln Ala Asn Asp Ile Pro Thr Asp Leu Val Lys  
 20 25 30  
 Ala Ile Val Ser Ile Glu Asp His Arg Phe Phe Asp His Arg Gly Ile  
 35 40 45  
 Asp Thr Ile Arg Ile Leu Gly Ala Phe Leu Arg Asn Leu Gln Ser Asn  
 50 55 60  
 Ser Leu Gln Gly Gly Ser Thr Leu Thr Gln Gln Leu Ile Lys Leu Thr  
 65 70 75 80  
 Tyr Phe Ser Thr Ser Thr Ser Asp Gln Thr Ile Ser Arg Lys Ala Gln  
 85 90 95  
 Glu Ala Trp Leu Ala Ile Gln Leu Glu Gln Lys Ala Thr Lys Gln Glu  
 100 105 110  
 Ile Leu Thr Tyr Tyr Ile Asn Lys Val Tyr Met Ser Asn Gly Asn Tyr  
 115 120 125  
 Gly Met Gln Thr Ala Ala Gln Asn Tyr Tyr Gly Lys Asp Leu Asn Asn  
 130 135 140  
 Leu Ser Leu Pro Gln Leu Ala Leu Leu Ala Gly Met Pro Gln Ala Pro  
 145 150 155 160  
 Asn Gln Tyr Asp Pro Tyr Ser His Pro Glu Ala Ala Gln Asp Arg Arg  
 165 170 175  
 Asn Leu Val Leu Ser Glu Met Lys Asn Gln Gly Tyr Ile Ser Ala Glu  
 180 185 190  
 Gln Tyr Glu Lys Ala Val Asn Thr Pro Ile Thr Asp Gly Leu Gln Ser  
 195 200 205  
 Leu Lys Ser Ala Ser Asn Tyr Pro Ala Tyr Met Asp Asn Tyr Leu Lys  
 210 215 220  
 Glu Val Ile Asn Gln Val Glu Glu Glu Thr Gly Tyr Asn Leu Leu Thr

225		230		235		240
Thr Gly Met Asp Val Tyr Thr Asn Val Asp Gln Glu Ala Gln Lys His	245		250		255	
Leu Trp Asp Ile Tyr Asn Thr Asp Glu Tyr Val Ala Tyr Pro Asp Asp	260		265		270	
Glu Leu Gln Val Ala Ser Thr Ile Val Asp Val Ser Asn Gly Lys Val	275		280		285	
Ile Ala Gln Leu Gly Ala Arg His Gln Ser Ser Asn Val Ser Phe Gly	290		295		300	
Ile Asn Gln Ala Val Glu Thr Asn Arg Asp Trp Gly Ser Thr Met Lys	305		310		315	320
Pro Ile Thr Asp Tyr Ala Pro Ala Leu Glu Tyr Gly Val Tyr Asp Ser	325		330		335	
Thr Ala Thr Ile Val His Asp Glu Pro Tyr Asn Tyr Pro Gly Thr Asn	340		345		350	
Thr Pro Val Tyr Asn Trp Asp Arg Gly Tyr Phe Gly Asn Ile Thr Leu	355		360		365	
Gln Tyr Ala Leu Gln Gln Ser Arg Asn Val Pro Ala Val Glu Thr Leu	370		375		380	
Asn Lys Val Gly Leu Asn Arg Ala Lys Thr Phe Leu Asn Gly Leu Gly	385		390		395	400
Ile Asp Tyr Pro Ser Ile His Tyr Ser Asn Ala Ile Ser Ser Asn Thr	405		410		415	
Thr Glu Ser Asp Lys Lys Tyr Gly Ala Ser Ser Glu Lys Met Ala Ala	420		425		430	
Ala Tyr Ala Ala Phe Ala Asn Gly Gly Thr Tyr Tyr Lys Pro Met Tyr	435		440		445	
Ile His Lys Val Val Phe Ser Asp Gly Ser Glu Lys Glu Phe Ser Asn	450		455		460	
Val Gly Thr Arg Ala Met Lys Glu Thr Thr Ala Tyr Met Met Thr Asp	465		470		475	480
Met Met Lys Thr Val Leu Thr Tyr Gly Thr Gly Arg Asn Ala Tyr Leu	485		490		495	
Ala Trp Leu Pro Gln Ala Gly Lys Thr Gly Thr Ser Asn Tyr Thr Asp	500		505		510	
Glu Glu Ile Glu Asn His Ile Lys Thr Ser Gln Phe Val Ala Pro Asp	515		520		525	
Glu Leu Phe Ala Gly Tyr Thr Arg Lys Tyr Ser Met Ala Val Trp Thr	530		535		540	
Gly Tyr Ser Asn Arg Leu Thr Pro Leu Val Gly Asn Gly Leu Thr Val	545		550		555	560
Ala Ala Lys Val Tyr Arg Ser Met Met Thr Tyr Leu Ser Glu Gly Ser	565		570		575	

Asn Pro Glu Asp Trp Asn Ile Pro Glu Gly Leu Tyr Arg Asn Gly Glu  
 580 585 590  
 Phe Val Phe Lys Asn Gly Ala Arg Ser Thr Trp Asn Ser Pro Ala Pro  
 595 600 605  
 Gln Gln Pro Pro Ser Thr Glu Ser Ser Ser Ser Ser Ser Asp Ser Ser  
 610 615 620  
 Thr Ser Gln Ser Ser Ser Thr Thr Pro Ser Thr Asn Asn Ser Thr Thr  
 625 630 635 640  
 Thr Asn Pro Asn Asn Asn Thr Gln Gln Ser Asn Thr Thr Pro Asp Gln  
 645 650 655  
 Gln Asn Gln Asn Pro Gln Pro Ala Gln Pro  
 660 665

## (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1714 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAATTACAAT ACGGACTATG AATTGACCTC TGGAGAAAAA TTACCTCTTC CTAAAGAGAT	60
TTCAGGTTAC ACTTATATTG GATATATCAA AGAGGGAAAA ACGACTTCTG AGTCTGAAGT	120
AAGTAATCAA AAGAGTTCAG TTGCCACTCC TACAAAACAA CAAAAGGTGG ATTATAATGT	180
TACACCGAAT TTTGTAGACC ATCCATCAAC AGTACAAGCT ATTCAGGAAC AAACACCTGT	240
TTCTTCAACT AAGCCGACAG AAGTTCAAGT AGTTGAAAAA CCTTTCTCTA CTGAATTAAT	300
CAATCCAAGA AAAGAAGAGA AACAATCTTC AGATTCTCAA GAACAATTAG CCGAACATAA	360
GAATCTAGAA ACGAAGAAAG AGGAGAAGAT TTCTCCAAAA GAAAAGACTG GGGTAAATAC	420
ATTAAATCCA CAGGATGAAG TTTTATCAGG TCAATTGAAC AAACCTGAAC TCTTATATCG	480
TGAGGAAACT ATGGAGACAA AAATAGATTT TCAAGAAGAA ATTCAAGAAA ATCCTGATTT	540
AGCTGAAGGA ACTGTAAGAG TAAAACAAGA AGGTAAATTA GGTAAGAAAG TTGAAATCGT	600
CAGAATATTC TCTGTAAACA AGGAAGAAGT TTCGCGAGAA ATTGTTTCAA CTTCAACGAC	660
TGCGCCTAGT CCAAGAATAG TCGAAAAAGG TACTAAAAAA ACTCAAGTTA TAAAGGAACA	720
ACCTGAGACT GGTGTAGAAC ATAAGGACGT ACAGTCTGGA GCTATTGTTG AACCCGCAAT	780
TCAGCCTGAG TTGCCCGAAG CTGTAGTAAG TGACAAAGGC GAACCAGAAG TTCAACCTAC	840
ATTACCCGAA GCAGTTGTGA CCGACAAAGG TGAGACTGAG GTTCAACCAG AGTCGCCAGA	900
TACTGTGGTA AGTGATAAAG GTGAACCAGA GCAGGTAGCA CCGCTTCCAG AATATAAGGG	960
TAATATTGAG CAAGTAAAC CTGAAACTCC GGTTGAGAAG ACCAAAGAAC AAGGTCCAGA	1020

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AAAAACTGAA GAAGTTCCAG TAAAACCAAC AGAAGAAACA CCAGTAAATC CAAATGAAGG      1080
TACTACAGAA GGAACCTCAA TTCAAGAAGC AGAAAATCCA GTTCAACCTG CAGAAGAATC      1140
AACAAACGAAT TCAGAGAAAAG TATCACCAGA TACATCTAGC AAAAATACTG GGAAGTGTGTC    1200
CAGTAATCCT AGTGATTCTG CAACCTCAGT TGGAGAATCA AATAAACCCAG AACATAATGA      1260
CTCTAAAAAT GAAAATTCTG AAAAACTGT AGAAGAAGTT CCAGTAAATC CAAATGAAGG      1320
CACAGTAGAA GGTACCTCAA ATCAAGAAAC AGAAAAACCA GTTCAACCTG CAGAAGAAAC      1380
ACAAACAAAC TCTGGGAAAA TAGCTAACGA AAATACTGGA GAAGTATCCA ATAAACCTAG      1440
TGATTCAAAA CCACCAAGTTG AAGAATCAAA TCAACCAGAA AAAAACGGAA CTGCAACAAA      1500
ACCAGAAAAAT TCAGGTAATA CAACATCAGA GAATGGACAA ACAGAACCAG AACCATCAAA      1560
CGGAAATTCA ACTGAGGATG TTTCAACCGA ATCAAACACA TCCAATTCAA ATGGAAACGA      1620
AGAAATTAAA CAAGAAAATG AACTAGACCC TGATAAAAAG GTAGAAGAAC CAGAGAAAAC      1680
ACTTGAATTA AGAAATGTTT CCGACCTAGA GTTA                                  1714

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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 571 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Asn Tyr Asn Thr Asp Tyr Glu Leu Thr Ser Gly Glu Lys Leu Pro Leu
1          5          10          15
Pro Lys Glu Ile Ser Gly Tyr Thr Tyr Ile Gly Tyr Ile Lys Glu Gly
20        25        30
Lys Thr Thr Ser Glu Ser Glu Val Ser Asn Gln Lys Ser Ser Val Ala
35        40        45
Thr Pro Thr Lys Gln Gln Lys Val Asp Tyr Asn Val Thr Pro Asn Phe
50        55        60
Val Asp His Pro Ser Thr Val Gln Ala Ile Gln Glu Gln Thr Pro Val
65        70        75        80
Ser Ser Thr Lys Pro Thr Glu Val Gln Val Val Glu Lys Pro Phe Ser
85        90        95
Thr Glu Leu Ile Asn Pro Arg Lys Glu Glu Lys Gln Ser Ser Asp Ser
100       105       110
Gln Glu Gln Leu Ala Glu His Lys Asn Leu Glu Thr Lys Lys Glu Glu
115       120       125
Lys Ile Ser Pro Lys Glu Lys Thr Gly Val Asn Thr Leu Asn Pro Gln
130       135       140

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Asp Glu Val Leu Ser Gly Gln Leu Asn Lys Pro Glu Leu Leu Tyr Arg  
 145 150 155 160  
 Glu Glu Thr Met Glu Thr Lys Ile Asp Phe Gln Glu Glu Ile Gln Glu  
 165 170 175  
 Asn Pro Asp Leu Ala Glu Gly Thr Val Arg Val Lys Gln Glu Gly Lys  
 180 185 190  
 Leu Gly Lys Lys Val Glu Ile Val Arg Ile Phe Ser Val Asn Lys Glu  
 195 200 205  
 Glu Val Ser Arg Glu Ile Val Ser Thr Ser Thr Thr Ala Pro Ser Pro  
 210 215 220  
 Arg Ile Val Glu Lys Gly Thr Lys Lys Thr Gln Val Ile Lys Glu Gln  
 225 230 235 240  
 Pro Glu Thr Gly Val Glu His Lys Asp Val Gln Ser Gly Ala Ile Val  
 245 250 255  
 Glu Pro Ala Ile Gln Pro Glu Leu Pro Glu Ala Val Val Ser Asp Lys  
 260 265 270  
 Gly Glu Pro Glu Val Gln Pro Thr Leu Pro Glu Ala Val Val Thr Asp  
 275 280 285  
 Lys Gly Glu Thr Glu Val Gln Pro Glu Ser Pro Asp Thr Val Val Ser  
 290 295 300  
 Asp Lys Gly Glu Pro Glu Gln Val Ala Pro Leu Pro Glu Tyr Lys Gly  
 305 310 315 320  
 Asn Ile Glu Gln Val Lys Pro Glu Thr Pro Val Glu Lys Thr Lys Glu  
 325 330 335  
 Gln Gly Pro Glu Lys Thr Glu Glu Val Pro Val Lys Pro Thr Glu Glu  
 340 345 350  
 Thr Pro Val Asn Pro Asn Glu Gly Thr Thr Glu Gly Thr Ser Ile Gln  
 355 360 365  
 Glu Ala Glu Asn Pro Val Gln Pro Ala Glu Glu Ser Thr Thr Asn Ser  
 370 375 380  
 Glu Lys Val Ser Pro Asp Thr Ser Ser Lys Asn Thr Gly Glu Val Ser  
 385 390 395 400  
 Ser Asn Pro Ser Asp Ser Thr Thr Ser Val Gly Glu Ser Asn Lys Pro  
 405 410 415  
 Glu His Asn Asp Ser Lys Asn Glu Asn Ser Glu Lys Thr Val Glu Glu  
 420 425 430  
 Val Pro Val Asn Pro Asn Glu Gly Thr Val Glu Gly Thr Ser Asn Gln  
 435 440 445  
 Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn Ser  
 450 455 460  
 Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro Ser  
 465 470 475 480

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 748 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TGAGAATCAA	GCTACACCCA	AAGAGACTAG	CGCTCAAAG	ACAATCGTCC	TTGCTACAGC	60
TGGCGACGTG	CCACCATTTC	ACTACGAAGA	CAAGGGCAAT	CTGACAGGCT	TTGATATCGA	120
AGTTTTTAAAG	GCAGTAGATG	AAAAACTCAG	CGACTACGAG	ATTCAATTCC	AAAGAACCGC	180
CTGGGAGAGC	ATCTTCCCAG	GACTTGATTTC	TGGTCACTAT	CAGGCTGCGG	CCAATAACTT	240
GAGTTACACA	AAAGAGCGTG	CTGAAAAATA	CCTTTACTCG	CTTCCAATTT	CCAACAATCC	300
CCTCGTCCTT	GTCAGCAACA	AGAAAAATCC	TTTGACTTCT	CTTGACCAGA	TCGCTGGTAA	360
AACAACACAA	GAGGATACCG	GAACTTCTAA	CGCTCAATTC	ATCAATAACT	GGAATCAGAA	420
ACACACTGAT	AATCCCGCTA	CAATTAATTT	TTCTGGTGAG	GATATTGGTA	AACGAATCCT	480
AGACCTTGCT	AACGGAGAGT	TTGATTTCTT	AGTTTTTGAC	AAGGTATCCG	TTCAAAAGAT	540
TATCAAGGAC	CGTGGTTTAG	ACCTCTCAGT	CGTTGATTTA	CCTTCTGCAG	ATAGCCCCAG	600
CAATTATATC	ATTTTCTCAA	GCGACCAAAA	AGAGTTTAAA	GAGCAATTTG	ATAAAGCGCT	660
CAAAGAACTC	TATCAAGACG	GAACCCTTGA	AAAACTCAGC	AATACCTATC	TAGGTGGTTC	720
TTACCTCCCA	GATCAATCTC	AGTTACAA				748

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Glu Asn Gln Ala Thr Pro Lys Glu Thr Ser Ala Gln Lys Thr Ile Val
1          5          10          15
Leu Ala Thr Ala Gly Asp Val Pro Pro Phe Asp Tyr Glu Asp Lys Gly
          20          25          30
Asn Leu Thr Gly Phe Asp Ile Glu Val Leu Lys Ala Val Asp Glu Lys
          35          40          45
Leu Ser Asp Tyr Glu Ile Gln Phe Gln Arg Thr Ala Trp Glu Ser Ile
          50          55          60
Phe Pro Gly Leu Asp Ser Gly His Tyr Gln Ala Ala Ala Asn Asn Leu
          65          70          75          80
Ser Tyr Thr Lys Glu Arg Ala Glu Lys Tyr Leu Tyr Ser Leu Pro Ile
          85          90          95
Ser Asn Asn Pro Leu Val Leu Val Ser Asn Lys Lys Asn Pro Leu Thr
          100          105          110
Ser Leu Asp Gln Ile Ala Gly Lys Thr Thr Gln Glu Asp Thr Gly Thr
          115          120          125
Ser Asn Ala Gln Phe Ile Asn Asn Trp Asn Gln Lys His Thr Asp Asn
          130          135          140
Pro Ala Thr Ile Asn Phe Ser Gly Glu Asp Ile Gly Lys Arg Ile Leu
          145          150          155          160
Asp Leu Ala Asn Gly Glu Phe Asp Phe Leu Val Phe Asp Lys Val Ser
          165          170          175
Val Gln Lys Ile Ile Lys Asp Arg Gly Leu Asp Leu Ser Val Val Asp
          180          185          190
Leu Pro Ser Ala Asp Ser Pro Ser Asn Tyr Ile Ile Phe Ser Ser Asp
          195          200          205
Gln Lys Glu Phe Lys Glu Gln Phe Asp Lys Ala Leu Lys Glu Leu Tyr
          210          215          220
Gln Asp Gly Thr Leu Glu Lys Leu Ser Asn Thr Tyr Leu Gly Gly Ser
          225          230          235          240
Tyr Leu Pro Asp Gln Ser Gln Leu Gln
          245

```

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 985 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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TGGTAACCGC TCTTCTCGTA ACGCAGCTTC ATCTTCTGAT GTGAAGACAA AAGCAGCAAT      60
CGTCACTGAT ACTGGTGGTG TTGATGACAA ATCATTCAAC CAATCAGCTT GGAAGGTTT      120
GCAGGCTTGG GGTAAAGAAC ACAATCTTTC AAAAGATAAC GGTTTCACTT ACTTCCAATC      180
AACAAAGTAA GCTGACTACG CTAACAACCTT GCAACAAGCG GCTGGAAGTT ACAACCTAAT      240
CTTCGGTGTT GGTTTTGCCC TTAATAATGC AGTTAAAGAT GCAGCAAAAAG AACACACTGA      300
CTTGAACCTAT GTCTTGATTG ATGATGTGAT TAAAGACCAA AAGAATGTTG CGAGCGTAAC      360
TTTCGCTGAT AATGAGTCAG GTTACCTTGC AGGTGTGGCT GCAGCAAAAA CAACTAAGAC      420
AAAACAAGTT GGTTTTGTAG GTGGTATCGA ATCTGAAGTT ATCTCTCGTT TTGAAGCAGG      480
ATTCAAGGCT GGTGTTGCGT CAGTAGACCC ATCTATCAAA GTCCAAGTTG ACTACGCTGG      540
TTCATTTGGT GATGCGGCTA AAGGTAAAAC AATTGCAGCC GCACAATACG CAGCCGGTGC      600
AGATATTGTT TACCAAGTAG CTGGTGGTAC AGGTGCAGGT GTCTTTGCAG AGGCAAAATC      660
TCTCAACGAA AGCCGTCCTG AAAATGAAAA AGTTTGGGTT ATCGGTGTTG ATCGTGACCA      720
AGAAGCAGAA GGTAAATACA CTTCTAAAGA TGGCAAAGAA TCAAACCTTG TTCTTGATC      780
TACTTTGAAA CAAGTTGGTA CAACTGTAAA AGATATTTCT AACAAGGCAG AAAGAGGAGA      840
ATTCCCTGGC GGTCAAGTGA TCGTTTACTC ATTGAAGGAT AAAGGGGTTG ACTTGCCAGT      900
AACAAACCTT TCAGAAGAAG GTAAAAAAGC TGTCGAAGAT GCAAAAGCTA AAATCCTTGA      960
TGGAAGCGTA AAAGTTCCTG AAAAA

```

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Gly Asn Arg Ser Ser Arg Asn Ala Ala Ser Ser Ser Asp Val Lys Thr
1          5          10          15
Lys Ala Ala Ile Val Thr Asp Thr Gly Gly Val Asp Asp Lys Ser Phe
20          25          30
Asn Gln Ser Ala Trp Glu Gly Leu Gln Ala Trp Gly Lys Glu His Asn
35          40          45
Leu Ser Lys Asp Asn Gly Phe Thr Tyr Phe Gln Ser Thr Ser Glu Ala
50          55          60
Asp Tyr Ala Asn Asn Leu Gln Gln Ala Ala Gly Ser Tyr Asn Leu Ile
65          70          75          80
Phe Gly Val Gly Phe Ala Leu Asn Asn Ala Val Lys Asp Ala Ala Lys
85          90          95

```

Glu His Thr Asp Leu Asn Tyr Val Leu Ile Asp Asp Val Ile Lys Asp  
 100 105 110  
 Gln Lys Asn Val Ala Ser Val Thr Phe Ala Asp Asn Glu Ser Gly Tyr  
 115 120 125  
 Leu Ala Gly Val Ala Ala Ala Lys Thr Thr Lys Thr Lys Gln Val Gly  
 130 135 140  
 Phe Val Gly Gly Ile Glu Ser Glu Val Ile Ser Arg Phe Glu Ala Gly  
 145 150 155 160  
 Phe Lys Ala Gly Val Ala Ser Val Asp Pro Ser Ile Lys Val Gln Val  
 165 170 175  
 Asp Tyr Ala Gly Ser Phe Gly Asp Ala Ala Lys Gly Lys Thr Ile Ala  
 180 185 190  
 Ala Ala Gln Tyr Ala Ala Gly Ala Asp Ile Val Tyr Gln Val Ala Gly  
 195 200 205  
 Gly Thr Gly Ala Gly Val Phe Ala Glu Ala Lys Ser Leu Asn Glu Ser  
 210 215 220  
 Arg Pro Glu Asn Glu Lys Val Trp Val Ile Gly Val Asp Arg Asp Gln  
 225 230 235 240  
 Glu Ala Glu Gly Lys Tyr Thr Ser Lys Asp Gly Lys Glu Ser Asn Phe  
 245 250 255  
 Val Leu Val Ser Thr Leu Lys Gln Val Gly Thr Thr Val Lys Asp Ile  
 260 265 270  
 Ser Asn Lys Ala Glu Arg Gly Glu Phe Pro Gly Gly Gln Val Ile Val  
 275 280 285  
 Tyr Ser Leu Lys Asp Lys Gly Val Asp Leu Ala Val Thr Asn Leu Ser  
 290 295 300  
 Glu Glu Gly Lys Lys Ala Val Glu Asp Ala Lys Ala Lys Ile Leu Asp  
 305 310 315 320  
 Gly Ser Val Lys Val Pro Glu Lys  
 325

## (2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGTGGAAATT TGACAGGTAA CAGCAAAAAA GCTGCTGATT CAGGTGACAA ACCTGTTATC	60
AAAATGTACC AAATCGGTGA CAAACCAGAC AACTTGATG AATTGTTAGC AAATGCCAAC	120
AAAATCATTG AAGAAAAAGT TGGTGCCAAA TTGGATATCC AATACCTTGG CTGGGGTGAC	180
TATGGTAAGA AAATGTCAGT TATCACATCA TCTGGTGAAG ACTATGATAT TGCCTTTGCA	240

GATAACTATA TTGTAAATGC TCAAAAAGGT GCTTACGCTG ACTTGACAGA ATTGTACAAA	300
AAAGAAGGTA AAGACCTTTA CAAAGCACTT GACCCAGCTT ACATCAAGGG TAATACTGTA	360
AATGGTAAGA TTTACGCTGT TCCAGTTGCA GCCAACGTTG CATCATCTCA AAACCTTTGCC	420
TTCAACGGAA CTCTCCTTGC TAAATATGGT ATCGATATTT CAGGTGTTAC TTCTTACGAA	480
ACTCTTGAGC CAGTCTTGAA ACAAATCAAA GAAAAAGCTC CAGACGTAGT ACCATTTGCT	540
ATTGGTAAAG TTTTCATCCC ATCTGATAAT TTTGACTACC CAGTAGCAAA CGGTCTTCCA	600
TTCGTTATCG ACCTTGAAGG CGATACTACT AAAGTTGTAA ACCGTTACGA AGTGCCTCGT	660
TTCAAAGAAC ACTTGAAGAC TCTTCACAAA TTCTATGAAG CTGGCTACAT TCCAAAAGAC	720
GTCGCAACAA GCGATACTTC CTTTGACCTT CAACAAGATA CTTGGTTCGT TCGTGAAGAA	780
ACAGTAGGAC CAGCTGACTA CGGTAACAGC TTGCTTTTAC GTGTTGCCAA CAAAGATATC	840
CAAATCAAAC CAATTACTAA CTTTCATCAAG NAAAACCAAA CAACACAAGT TGCTAACTTT	900
GTCATCTCAA ACAACTCTAA GAACAAAGAA AAATCAATGG AAATCTTGAA CCTCTTGAAT	960
ACGAACCCAG AACTCTTGAA CGGTCTTGTT TACGGTCCAG AAGGCAAGAA CTGGGAAAAA	1020
ATTGAAGGTA AAGAAAACCG TGTTGCGGTT CTTGATGGCT ACAAAGGAAA CACTCACATG	1080
GGTGGATGGA ACACTGGTAA CAACTGGATC CTTTACATCA ACGAAAACGT TACAGACCAA	1140
CAAATCGAAA ATTCTAAGAA AGAATTGGCA GAAGCTAAAG AATCTCCAGC GCTTGGATTT	1200
ATCTTCAATA CTGACAATGT GAAATCTGAA ATCTCAGCTA TTGCTAACAC AATGCAACAA	1260
TTTGATACAG CTATCAACAC TGGTACTGTA GACCCAGATA AAGCGATTCC AGAATTGATG	1320
GAAAAATTGA AATCTGAAGG TGCCTACGAA AAAGTATTGA ACGAAATGCA AAAACAATAC	1380
GATGAATTCT TGAAAAACAA AAAA	1404

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 468 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys	Gly	Asn	Leu	Thr	Gly	Asn	Ser	Lys	Lys	Ala	Ala	Asp	Ser	Gly	Asp
1				5					10					15	
Lys	Pro	Val	Ile	Lys	Met	Tyr	Gln	Ile	Gly	Asp	Lys	Pro	Asp	Asn	Leu
			20				25						30		
Asp	Glu	Leu	Leu	Ala	Asn	Ala	Asn	Lys	Ile	Ile	Glu	Glu	Lys	Val	Gly
		35				40					45				
Ala	Lys	Leu	Asp	Ile	Gln	Tyr	Leu	Gly	Trp	Gly	Asp	Tyr	Gly	Lys	Lys

50					55					60					
Met 65	Ser	Val	Ile	Thr	Ser 70	Ser	Gly	Glu	Asn	Tyr 75	Asp	Ile	Ala	Phe	Ala 80
Asp	Asn	Tyr	Ile	Val 85	Asn	Ala	Gln	Lys	Gly 90	Ala	Tyr	Ala	Asp	Leu 95	Thr
Glu	Leu	Tyr	Lys 100	Lys	Glu	Gly	Lys	Asp 105	Leu	Tyr	Lys	Ala	Leu 110	Asp	Pro
Ala	Tyr	Ile 115	Lys	Gly	Asn	Thr	Val 120	Asn	Gly	Lys	Ile	Tyr 125	Ala	Val	Pro
Val 130	Ala	Ala	Asn	Val	Ala	Ser 135	Ser	Gln	Asn	Phe	Ala 140	Phe	Asn	Gly	Thr
Leu 145	Leu	Ala	Lys	Tyr	Gly 150	Ile	Asp	Ile	Ser	Gly 155	Val	Thr	Ser	Tyr	Glu 160
Thr	Leu	Glu	Pro	Val 165	Leu	Lys	Gln	Ile	Lys 170	Glu	Lys	Ala	Pro	Asp 175	Val
Val	Pro	Phe	Ala 180	Ile	Gly	Lys	Val	Phe 185	Ile	Pro	Ser	Asp	Asn 190	Phe	Asp
Tyr	Pro	Val 195	Ala	Asn	Gly	Leu	Pro 200	Phe	Val	Ile	Asp	Leu 205	Glu	Gly	Asp
Thr 210	Thr	Lys	Val	Val	Asn	Arg 215	Tyr	Glu	Val	Pro	Arg 220	Phe	Lys	Glu	His
Leu 225	Lys	Thr	Leu	His	Lys 230	Phe	Tyr	Glu	Ala	Gly 235	Tyr	Ile	Pro	Lys	Asp 240
Val	Ala	Thr	Ser	Asp 245	Thr	Ser	Phe	Asp	Leu 250	Gln	Gln	Asp	Thr	Trp 255	Phe
Val	Arg	Glu	Glu 260	Thr	Val	Gly	Pro	Ala 265	Asp	Tyr	Gly	Asn	Ser 270	Leu	Leu
Ser	Arg	Val 275	Ala	Asn	Lys	Asp	Ile 280	Gln	Ile	Lys	Pro	Ile 285	Thr	Asn	Phe
Ile	Lys 290	Xaa	Asn	Gln	Thr	Thr 295	Gln	Val	Ala	Asn	Phe 300	Val	Ile	Ser	Asn
Asn 305	Ser	Lys	Asn	Lys	Glu 310	Lys	Ser	Met	Glu	Ile 315	Leu	Asn	Leu	Leu	Asn 320
Thr	Asn	Pro	Glu	Leu 325	Leu	Asn	Gly	Leu	Val 330	Tyr	Gly	Pro	Glu	Gly 335	Lys
Asn	Trp	Glu	Lys 340	Ile	Glu	Gly	Lys	Glu 345	Asn	Arg	Val	Arg	Val 350	Leu	Asp
Gly	Tyr	Lys 355	Gly	Asn	Thr	His	Met 360	Gly	Gly	Trp	Asn	Thr 365	Gly	Asn	Asn
Trp 370	Ile	Leu	Tyr	Ile	Asn	Glu 375	Asn	Val	Thr	Asp	Gln 380	Gln	Ile	Glu	Asn
Ser 385	Lys	Lys	Glu	Leu	Ala 390	Glu	Ala	Lys	Glu	Ser 395	Pro	Ala	Leu	Gly	Phe 400

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 937 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TGGTCAAGGA	ACTGCTTCTA	AAGACAACAA	AGAGGCAGAA	CTTAAGAAAGG	TTGACTTTAT	60
CCTAGACTGG	ACACCAAATA	CCAACCACAC	AGGGCTTTAT	GTTGCCAAGG	AAAAAGGTTA	120
TTTCAAAGAA	GCTGGAGTGG	ATGTTGATTT	GAAATTGCCA	CCAGAAGAAA	GTTCTTCTGA	180
CTTGGTTATC	AACGGAAAGG	CACCATTTGC	AGTGTATTTT	CAAGACTACA	TGGCTAAGAA	240
ATTGGAAAAA	GGAGCAGGAA	TCACTGCCGT	TGCAGCTATT	GTTGAACACA	ATACATCAGG	300
AATCATCTCT	CGTAAATCTG	ATAATGTAAG	CAGTCCAAAA	GACTTGGTTG	GTAAGAAATA	360
TGGGACATGG	AATGACCCAA	CTGAACTTGC	TATGTTGAAA	ACCTTGGTAG	AATCTCAAGG	420
TGGAGACTTT	GAGAAGGTTG	AAAAAGTACC	AAATAACGAC	TCAAACCTCA	TCACACCGAT	480
TGCCAATGGC	GTCTTTGATA	CTGCTTGGAT	TTACTACGGT	TGGGATGGTA	TCCTTGCTAA	540
ATCTCAAGGT	GTAGATGCTA	ACTTCATGTA	CTTGAAAGAC	TATGTCAAGG	AGTTTGACTA	600
CTATTCACCA	GTTATCATCG	CAAACAACGA	CTATCTGAAA	GATAACAAAG	AAGAAGCTCG	660
CAAAGTCATC	CAAGCCATCA	AAAAAGGCTA	CCAATATGCC	ATGGAACATC	CAGAAGAAGC	720
TGCAGATATT	CTCATCAAGA	ATGCACCTGA	ACTCAAGGAA	AAACGTGACT	TTGTCATCGA	780
ATCTCAAAAA	TACTTGTCAA	AAGAATACGC	AAGCGACAAG	GAAAAATGGG	GTCAATTTGA	840
CGCAGCTCGC	TGGAATGCTT	TCTACAAATG	GGATAAAGAA	AATGGTATCC	TTAAAGAAGA	900
CTTGACAGAC	AAAGGCTTCA	CCAACGAATT	TGTGAAA			937

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 312 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly	Gln	Gly	Thr	Ala	Ser	Lys	Asp	Asn	Lys	Glu	Ala	Glu	Leu	Lys	Lys	1	5	10	15
Val	Asp	Phe	Ile	Leu	Asp	Trp	Thr	Pro	Asn	Thr	Asn	His	Thr	Gly	Leu	20	25	30	
Tyr	Val	Ala	Lys	Glu	Lys	Gly	Tyr	Phe	Lys	Glu	Ala	Gly	Val	Asp	Val	35	40	45	
Asp	Leu	Lys	Leu	Pro	Pro	Glu	Glu	Ser	Ser	Ser	Asp	Leu	Val	Ile	Asn	50	55	60	
Gly	Lys	Ala	Pro	Phe	Ala	Val	Tyr	Phe	Gln	Asp	Tyr	Met	Ala	Lys	Lys	65	70	75	80
Leu	Glu	Lys	Gly	Ala	Gly	Ile	Thr	Ala	Val	Ala	Ala	Ile	Val	Glu	His	85	90	95	
Asn	Thr	Ser	Gly	Ile	Ile	Ser	Arg	Lys	Ser	Asp	Asn	Val	Ser	Ser	Pro	100	105	110	
Lys	Asp	Leu	Val	Gly	Lys	Lys	Tyr	Gly	Thr	Trp	Asn	Asp	Pro	Thr	Glu	115	120	125	
Leu	Ala	Met	Leu	Lys	Thr	Leu	Val	Glu	Ser	Gln	Gly	Gly	Asp	Phe	Glu	130	135	140	
Lys	Val	Glu	Lys	Val	Pro	Asn	Asn	Asp	Ser	Asn	Ser	Ile	Thr	Pro	Ile	145	150	155	160
Ala	Asn	Gly	Val	Phe	Asp	Thr	Ala	Trp	Ile	Tyr	Tyr	Gly	Trp	Asp	Gly	165	170	175	
Ile	Leu	Ala	Lys	Ser	Gln	Gly	Val	Asp	Ala	Asn	Phe	Met	Tyr	Leu	Lys	180	185	190	
Asp	Tyr	Val	Lys	Glu	Phe	Asp	Tyr	Tyr	Ser	Pro	Val	Ile	Ile	Ala	Asn	195	200	205	
Asn	Asp	Tyr	Leu	Lys	Asp	Asn	Lys	Glu	Glu	Ala	Arg	Lys	Val	Ile	Gln	210	215	220	
Ala	Ile	Lys	Lys	Gly	Tyr	Gln	Tyr	Ala	Met	Glu	His	Pro	Glu	Glu	Ala	225	230	235	240
Ala	Asp	Ile	Leu	Ile	Lys	Asn	Ala	Pro	Glu	Leu	Lys	Glu	Lys	Arg	Asp	245	250	255	
Phe	Val	Ile	Glu	Ser	Gln	Lys	Tyr	Leu	Ser	Lys	Glu	Tyr	Ala	Ser	Asp	260	265	270	
Lys	Glu	Lys	Trp	Gly	Gln	Phe	Asp	Ala	Ala	Arg	Trp	Asn	Ala	Phe	Tyr	275	280	285	
Lys	Trp	Asp	Lys	Glu	Asn	Gly	Ile	Leu	Lys	Glu	Asp	Leu	Thr	Asp	Lys	290	295	300	

Gly Phe Thr Asn Glu Phe Val Lys  
305 310

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 799 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TAGCTCAGGT GGAAACGCTG GTTCATCCTC TGGAAAAACA ACTGCCAAAG CTCGCACTAT	60
CGATGAAATC AAAAAAAGCG GTGAAGTGGC AATCGCCGTG TTTGGAGATA AAAAACCGTT	120
TGGCTACGTT GACAATGATG GTTCTACCAA GGTACGCTAC GATATTGAAC TAGGGAACCA	180
ACTAGCTCAA GACCTTGGTG TCAAGGTAA ATACATTTCA GTCGATGCTG CCAACCGTGC	240
GGAATACTTG ATTTCAAACA AGGTAGATAT TACTCTTGCT AACTTTACAG TAACTGACGA	300
ACGTAAGAAA CAAGTTGATT TTGCCCTTCC ATATATGAAA GTTTCTCTGG GTGTCGTATC	360
ACCTAAGACT GGTCTCATT AAGACGTCAA ACAACTTGAA GTTAAACCT TAATTGTCAC	420
AAAAGGAACG ACTGCTGAGA CTTATTTTGA AAAGAATCAT CCAGAAATCA AACTCCAAAA	480
ATACGACCAA TACAGTGAAT CTTACCAAGC TCTTCTTGAC GGACGTGGAG ATGCCTTTTC	540
AACTGACAAT ACGGAAGTTC TAGCTTGGGC GCTTGAAAAT AAAGGATTTG AAGTAGGAAT	600
TACTTCCCTC GGTGATCCCG ATACCATTGC GGCAGCAGTT CAAAAAGGCA ACCAAGAATT	660
GCTAGACTTC ATCAATAAAG ATATTGAAAA ATTAGGCAAG GAAAACTTCT TCCACAAGGC	720
CTATGAAAAG ACACTTCACC CAACCTACGG TGACGCTGCT AAAGCAGATG ACCTGGTTGT	780
TGAAGGTGGA AAAGTTGAT	799

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 266 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Ser Gly Gly Asn Ala Gly Ser Ser Ser Gly Lys Thr Thr Ala Lys	
1 5 10 15	
Ala Arg Thr Ile Asp Glu Ile Lys Lys Ser Gly Glu Leu Arg Ile Ala	
20 25 30	
Val Phe Gly Asp Lys Lys Pro Phe Gly Tyr Val Asp Asn Asp Gly Ser	
35 40 45	

Thr Lys Val Arg Tyr Asp Ile Glu Leu Gly Asn Gln Leu Ala Gln Asp  
 50 55 60  
 Leu Gly Val Lys Val Lys Tyr Ile Ser Val Asp Ala Ala Asn Arg Ala  
 65 70 75 80  
 Glu Tyr Leu Ile Ser Asn Lys Val Asp Ile Thr Leu Ala Asn Phe Thr  
 85 90 95  
 Val Thr Asp Glu Arg Lys Lys Gln Val Asp Phe Ala Leu Pro Tyr Met  
 100 105 110  
 Lys Val Ser Leu Gly Val Val Ser Pro Lys Thr Gly Leu Ile Thr Asp  
 115 120 125  
 Val Lys Gln Leu Glu Gly Lys Thr Leu Ile Val Thr Lys Gly Thr Thr  
 130 135 140  
 Ala Glu Thr Tyr Phe Glu Lys Asn His Pro Glu Ile Lys Leu Gln Lys  
 145 150 155 160  
 Tyr Asp Gln Tyr Ser Asp Ser Tyr Gln Ala Leu Leu Asp Gly Arg Gly  
 165 170 175  
 Asp Ala Phe Ser Thr Asp Asn Thr Glu Val Leu Ala Trp Ala Leu Glu  
 180 185 190  
 Asn Lys Gly Phe Glu Val Gly Ile Thr Ser Leu Gly Asp Pro Asp Thr  
 195 200 205  
 Ile Ala Ala Ala Val Gln Lys Gly Asn Gln Glu Leu Leu Asp Phe Ile  
 210 215 220  
 Asn Lys Asp Ile Glu Lys Leu Gly Lys Glu Asn Phe Phe His Lys Ala  
 225 230 235 240  
 Tyr Glu Lys Thr Leu His Pro Thr Tyr Gly Asp Ala Ala Lys Ala Asp  
 245 250 255  
 Asp Leu Val Val Glu Gly Gly Lys Val Asp  
 260 265

## (2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1189 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCCAATCTAT GGTAAATCTG CGGATGGCAC AGTGACCATC GAGTATTTCA ACCAGAAAAA	60
AGAAATGACC AAAACCTTGG AAGAAATCAC TCGTGATTTT GAGAAGGAAA ACCCTAAGAT	120
CAAGGTCAAA GTCGTCAATG TACCAAATGC TGGTGAAGTA TTGAAGACAC GCGTTCTCGC	180
AGGAGATGTG CCTGATGTGG TCAATATTTA CCCACAGTCC ATCGAACTGC AAGAATGGGC	240
AAAAGCAGGT GTTTTGAAG ATTTGAGCAA CAAAGACTAC CTGAAACGCG TGAAAAATGG	300

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CTACGCTGAA AAATATGCTG TAAACGAAAA AGTTTACAAC GTTCCTTTTA CAGCTAATGC      360
TTATGGAATT TACTACAACA AAGATAAATT CGAAGAAGTG GGCTTGAAGG TTCCTGAAAC      420
CTGGGATGAA TTTGAACAGT TAGTCAAAGA TATCGTTGCT AAAGGACAAA CACCATTTGG      480
AATTGCAGGT GCAGATGCTT GGACACTCAA TGGTTACAAT CAATTAGCCT TTGCGACAGC      540
AACAGGTGGA GGAAAAGAAG CAAATCAATA CCTTCGTTAT TCTCAACCAA ATGCCATTAA      600
ATTGTCGGAT CCGATTATGA AAGATGATAT CAAGGTCATG GACATCCTTC GCATCAATGG      660
ATCTAAGCAA AAGAACTGGG AAGGTGCTGG CTATACCGAT GTTATCGGAG CCTTCGCACG      720
TGGGGATGTC CTCATGACAC CAAATGGGTC TTGGGCGATC ACAGCGATTA ATGAACAAAA      780
ACCGAACTTT AAGATTGGGA CCTTCATGAT TCCAGGAAAA GAAAAAGGAC AAAGCTTAAC      840
CGTTGGTGCG GGAGACTTGG CATGGTCTAT CTCAGCCACC ACCAAACATC CAAAAGAAGC      900
CAATGCCTTT GTGGAATATA TGACCCGTCC AGAAGTCATG CAAAAATACT ACGATGTGGA      960
CGGATCTCCA ACAGCGATCG AAGGGGTCAA ACAAGCAGGA GAAGATTCAC CGCTTGCTGG     1020
TATGACCGAA TATGCCTTTA CGGATCGTCA CTTGGTCTGG TTGCAACAAT ACTGGACCAG     1080
TGAAGCAGAC TTCCATACCT TGACCATGAA CTATGTCTTG ACCGGTGATA AACAAGGCAT     1140
GGTCAATGAT TTGAATGCCT TCTTTAACCC GATGAAAGCG GATGTGGAT      1189

```

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Ser Asn Tyr Gly Lys Ser Ala Asp Gly Thr Val Thr Ile Glu Tyr Phe
1          5          10          15
Asn Gln Lys Lys Glu Met Thr Lys Thr Leu Glu Glu Ile Thr Arg Asp
20        25        30
Phe Glu Lys Glu Asn Pro Lys Ile Lys Val Lys Val Val Asn Val Pro
35        40        45
Asn Ala Gly Glu Val Leu Lys Thr Arg Val Leu Ala Gly Asp Val Pro
50        55        60
Asp Val Val Asn Ile Tyr Pro Gln Ser Ile Glu Leu Gln Glu Trp Ala
65        70        75        80
Lys Ala Gly Val Phe Glu Asp Leu Ser Asn Lys Asp Tyr Leu Lys Arg
85        90        95
Val Lys Asn Gly Tyr Ala Glu Lys Tyr Ala Val Asn Glu Lys Val Tyr
100       105       110

```

Asn Val Pro Phe Thr Ala Asn Ala Tyr Gly Ile Tyr Tyr Asn Lys Asp  
           115                                  120                                  125  
 Lys Phe Glu Glu Leu Gly Leu Lys Val Pro Glu Thr Trp Asp Glu Phe  
           130                                  135                                  140  
 Glu Gln Leu Val Lys Asp Ile Val Ala Lys Gly Gln Thr Pro Phe Gly  
   145                                  150                                  155                                  160  
 Ile Ala Gly Ala Asp Ala Trp Thr Leu Asn Gly Tyr Asn Gln Leu Ala  
                                   165                                  170                                  175  
 Phe Ala Thr Ala Thr Gly Gly Gly Lys Glu Ala Asn Gln Tyr Leu Arg  
                                   180                                  185                                  190  
 Tyr Ser Gln Pro Asn Ala Ile Lys Leu Ser Asp Pro Ile Met Lys Asp  
           195                                  200                                  205  
 Asp Ile Lys Val Met Asp Ile Leu Arg Ile Asn Gly Ser Lys Gln Lys  
   210                                  215                                  220  
 Asn Trp Glu Gly Ala Gly Tyr Thr Asp Val Ile Gly Ala Phe Ala Arg  
   225                                  230                                  235                                  240  
 Gly Asp Val Leu Met Thr Pro Asn Gly Ser Trp Ala Ile Thr Ala Ile  
                                   245                                  250                                  255  
 Asn Glu Gln Lys Pro Asn Phe Lys Ile Gly Thr Phe Met Ile Pro Gly  
                                   260                                  265                                  270  
 Lys Glu Lys Gly Gln Ser Leu Thr Val Gly Ala Gly Asp Leu Ala Trp  
           275                                  280                                  285  
 Ser Ile Ser Ala Thr Thr Lys His Pro Lys Glu Ala Asn Ala Phe Val  
   290                                  295                                  300  
 Glu Tyr Met Thr Arg Pro Glu Val Met Gln Lys Tyr Tyr Asp Val Asp  
   305                                  310                                  315                                  320  
 Gly Ser Pro Thr Ala Ile Glu Gly Val Lys Gln Ala Gly Glu Asp Ser  
                                   325                                  330                                  335  
 Pro Leu Ala Gly Met Thr Glu Tyr Ala Phe Thr Asp Arg His Leu Val  
                                   340                                  345                                  350  
 Trp Leu Gln Gln Tyr Trp Thr Ser Glu Ala Asp Phe His Thr Leu Thr  
           355                                  360                                  365  
 Met Asn Tyr Val Leu Thr Gly Asp Lys Gln Gly Met Val Asn Asp Leu  
   370                                  375                                  380  
 Asn Ala Phe Phe Asn Pro Met Lys Ala Asp Val Asp  
   385                                  390                                  395

## (2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 775 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

TGGGAAAAAT TCTAGCGAAA CTAGTGGAGA TAATTGGTCA AAGTACCAGT CTAACAAGTC      60
TATTACTATT GGATTTGATA GTACTTTTGT TCCAATGGGA TTTGCTCAGA AAGATGGTTC      120
TTATGCAGGA TTTGATATTG ATTTAGCTAC AGCTGTTTTT GAAAAATACG GAATCACGGT      180
AAATTGGCAA CCGATTGATT GGGATTTGAA AGAAGCTGAA TTGACAAAAG GAACGATTGA      240
TCTGATTTGG AATGGCTATT CCGCTACAGA CGAACGCCGT GAAAAGGTGG CTTTCAGTAA      300
CTCATATATG AAGAATGAGC AGGTATTGGT TACGAAGAAA TCATCTGGTA TCACGACTGC      360
AAAGGATATG ACTGGAAAGA CATTAGGAGC TCAAGCTGGT TCATCTGGTT ATGCGGACTT      420
TGAAGCAAAT CCAGAAATTT TGAAGAATAT TGTCGCTAAT AAGGAAGCGA ATCAATACCA      480
AACCTTTAAT GAAGCCTTGA TTGATTTGAA AAACGATCGA ATTGATGGTC TATTGATTGA      540
CCGTGTCTAT GCAAACCTATT ATTTAGAAGC AGAAGGTGTT TTAAACGATT ATAATGTCTT      600
TACAGTTGGA CTAGAAACAG AAGCTTTTGC GGTGAGGCC CGTAAGGAAG ATACAACTT      660
GGTTAAGAAG ATAAATGAAG CTTTTTCTAG TCTTTACAAG GACGGCAAGT TCCAAGAAAT      720
CAGCCAAAAA TGGTTTGGAG AAGATGTAGC AACCAAAGAA GTAAAAGAAG GACAG      775

```

## (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 258 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

Gly Lys Asn Ser Ser Glu Thr Ser Gly Asp Asn Trp Ser Lys Tyr Gln
1          5          10          15
Ser Asn Lys Ser Ile Thr Ile Gly Phe Asp Ser Thr Phe Val Pro Met
20        25        30
Gly Phe Ala Gln Lys Asp Gly Ser Tyr Ala Gly Phe Asp Ile Asp Leu
35        40        45
Ala Thr Ala Val Phe Glu Lys Tyr Gly Ile Thr Val Asn Trp Gln Pro
50        55        60
Ile Asp Trp Asp Leu Lys Glu Ala Glu Leu Thr Lys Gly Thr Ile Asp
65        70        75        80
Leu Ile Trp Asn Gly Tyr Ser Ala Thr Asp Glu Arg Arg Glu Lys Val
85        90        95
Ala Phe Ser Asn Ser Tyr Met Lys Asn Glu Gln Val Leu Val Thr Lys
100       105       110
Lys Ser Ser Gly Ile Thr Thr Ala Lys Asp Met Thr Gly Lys Thr Leu
115      120      125

```

Gly Ala Gln Ala Gly Ser Ser Gly Tyr Ala Asp Phe Glu Ala Asn Pro  
 130 135 140  
 Glu Ile Leu Lys Asn Ile Val Ala Asn Lys Glu Ala Asn Gln Tyr Gln  
 145 150 155 160  
 Thr Phe Asn Glu Ala Leu Ile Asp Leu Lys Asn Asp Arg Ile Asp Gly  
 165 170 175  
 Leu Leu Ile Asp Arg Val Tyr Ala Asn Tyr Tyr Leu Glu Ala Glu Gly  
 180 185 190  
 Val Leu Asn Asp Tyr Asn Val Phe Thr Val Gly Leu Glu Thr Glu Ala  
 195 200 205  
 Phe Ala Val Gly Ala Arg Lys Glu Asp Thr Asn Leu Val Lys Lys Ile  
 210 215 220  
 Asn Glu Ala Phe Ser Ser Leu Tyr Lys Asp Gly Lys Phe Gln Glu Ile  
 225 230 235 240  
 Ser Gln Lys Trp Phe Gly Glu Asp Val Ala Thr Lys Glu Val Lys Glu  
 245 250 255  
 Gly Gln

## (2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 868 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGCTAGCGGA AAAAAAGATA CAACTTCTGG TCAAAAACTA AAAGTTGTTG CTACAAACTC	60
AATCATCGCT GATATTACTA AAAATATTGC TGGTGACAAA ATTGACCTTC ATAGTATCGT	120
TCCGATTGGG CAAGACCCAC ACGAATACGA ACCACTTCCT GAAGACGTTA AGAAAACTTC	180
TGAGGCTAAT TTGATTTTCT ATAACGGTAT CAACCTTGAA ACAGGTGGCA ATGCTTGTTT	240
TACAAAATTG GTAGAAAATG CCAAGAAAAC TGAAAACAAA GACTACTTCG CAGTCAGCGA	300
CGGCGTTGAT GTTATCTACC TTGAAGGTCA AAATGAAAAA GGAAAAGAAG ACCCACACGC	360
TTGGCTTAAC CTTGAAAACG GTATTATTTT TGCTAAAAAT ATCGCCAAAC AATTGAGCGC	420
CAAAGACCCT AACAATAAAG AATTCTATGA AAAAAATCTC AAAGAATATA CTGATAAGTT	480
AGACAAACTT GATAAAGAAA GTAAGGATAA ATTTAATAAG ATCCCTGCTG AAAAGAAACT	540
CATTGTAACC AGCGAAGGAG CATTCAAATA CTTCTCTAAA GCCTATGGTG TCCCAAGTGC	600
TTACATCTGG GAAATCAATA CTGAAGAAGA AGGAACTCCT GAACAAATCA AGACCTTGGT	660
TGAAAAACTT CGCCAAACAA AAGTTCCATC ACTCTTTGTA GAATCAAGTG TGGATGACCG	720
TCCAATGAAA ACTGTTTCTC AAGACACAAA CATCCCAATC TACGCTCAAA TCTTTACTGA	780

CTCTATCGCA GAACAAGGTA AAGAAGGCGA CAGCTACTAC AGCATGATGA AATACAACCT  
 TGACAAGATT GCTGAAGGAT TGGCAAAA

840

868

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala	Ser	Gly	Lys	Lys	Asp	Thr	Thr	Ser	Gly	Gln	Lys	Leu	Lys	Val	Val	1	5	10	15
Ala	Thr	Asn	Ser	Ile	Ile	Ala	Asp	Ile	Thr	Lys	Asn	Ile	Ala	Gly	Asp	20	25	30	
Lys	Ile	Asp	Leu	His	Ser	Ile	Val	Pro	Ile	Gly	Gln	Asp	Pro	His	Glu	35	40	45	
Tyr	Glu	Pro	Leu	Pro	Glu	Asp	Val	Lys	Lys	Thr	Ser	Glu	Ala	Asn	Leu	50	55	60	
Ile	Phe	Tyr	Asn	Gly	Ile	Asn	Leu	Glu	Thr	Gly	Gly	Asn	Ala	Trp	Phe	65	70	75	
Thr	Lys	Leu	Val	Glu	Asn	Ala	Lys	Lys	Thr	Glu	Asn	Lys	Asp	Tyr	Phe	85	90	95	
Ala	Val	Ser	Asp	Gly	Val	Asp	Val	Ile	Tyr	Leu	Glu	Gly	Gln	Asn	Glu	100	105	110	
Lys	Gly	Lys	Glu	Asp	Pro	His	Ala	Trp	Leu	Asn	Leu	Glu	Asn	Gly	Ile	115	120	125	
Ile	Phe	Ala	Lys	Asn	Ile	Ala	Lys	Gln	Leu	Ser	Ala	Lys	Asp	Pro	Asn	130	135	140	
Asn	Lys	Glu	Phe	Tyr	Glu	Lys	Asn	Leu	Lys	Glu	Tyr	Thr	Asp	Lys	Leu	145	150	155	
Asp	Lys	Leu	Asp	Lys	Glu	Ser	Lys	Asp	Lys	Phe	Asn	Lys	Ile	Pro	Ala	165	170	175	
Glu	Lys	Lys	Leu	Ile	Val	Thr	Ser	Glu	Gly	Ala	Phe	Lys	Tyr	Phe	Ser	180	185	190	
Lys	Ala	Tyr	Gly	Val	Pro	Ser	Ala	Tyr	Ile	Trp	Glu	Ile	Asn	Thr	Glu	195	200	205	
Glu	Glu	Gly	Thr	Pro	Glu	Gln	Ile	Lys	Thr	Leu	Val	Glu	Lys	Leu	Arg	210	215	220	
Gln	Thr	Lys	Val	Pro	Ser	Leu	Phe	Val	Glu	Ser	Ser	Val	Asp	Asp	Arg	225	230	235	
Pro	Met	Lys	Thr	Val	Ser	Gln	Asp	Thr	Asn	Ile	Pro	Ile	Tyr	Ala	Gln				

[illegible]

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1546 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TGGCTCAAAA	AATACAGCTT	CAAGTCCAGA	TTATAAGTTG	GAAGGTGTAA	CATTCCCGCT	60
TCAAGAAAAG	AAAACATTGA	AGTTTATGAC	AGCCAGTTCA	CCGTTATCTC	CTAAAGACCC	120
AAATGAAAAG	TTAATTTTGC	AACGTTTGGA	GAAGGAAACT	GGCGTTCATA	TTGACTGGAC	180
CAACTACCAA	TCCGACTTTG	CAGAAAAACG	TAAGTTGGAT	ATTTCTAGTG	GTGATTTACC	240
AGATGCTATC	CACAACGACG	GAGCTTCAGA	TGTGGACTTG	ATGAACTGGG	CTAAAAAAGG	300
TGTTATTATT	CCAGTTGAAG	ATTTGATTGA	TAAATACATG	CCAAATCTTA	AGAAAATTTT	360
GGATGAGAAA	CCAGAGTACA	AGGCCTTGAT	GACAGCACCT	GATGGGCACA	TTACTCATT	420
TCCATGGATT	GAAGAGCTTG	GAGATGGTAA	AGAGTCTATT	CACAGTGTCA	ACGATATGGC	480
TTGGATTAA	AAAGATTGGC	TTAAGAAACT	TGGTCTTGAA	ATGCCAAAAA	CTACTGATGA	540
TTTGATTAAA	GTCCTAGAAG	CTTTCAAAAA	CGGGGATCCA	AATGGAAATG	GAGAGGCTGA	600
TGAAATTCCA	TTTTCATTTA	TTAGTGGTAA	CGGAAACGAA	GATTTTAAAT	TCCTATTTGC	660
TGCATTTGGT	ATAGGGGATA	ACGATGATCA	TTTAGTAGTA	GGAAATGATG	GCAAAGTTGA	720
CTTCACAGCA	GATAACGATA	ACTATAAAGA	AGGTGTCAAA	TTTATCCGTC	AATTGCAAGA	780
AAAAGGCCTG	ATTGATAAAG	AAGCTTTTCGA	ACATGATTGG	AATAGTTACA	TTGCTAAAGG	840
TCATGATCAG	AAATTTGGTG	TTTACTTTAC	ATGGGATAAG	AATAATGTTA	CTGGAAGTAA	900
CGAAAGTTAT	GATGTTTTAC	CAGTACTTGC	TGGACCAAGT	GGTCAAAAAC	ACGTAGCTCG	960
TACAAACGGT	ATGGGATTTG	CACGTGACAA	GATGGTTATT	ACCAGTGTAA	ACAAAAACCT	1020
AGAATTGACA	GCTAAATGGA	TTGATGCACA	ATACGCTCCA	CTCCAATCTG	TGCAAAATAA	1080
CTGGGGAACT	TACGGAGATG	ACAAACAACA	AAACATCTTT	GAATTGGATC	AAGCGTCAAA	1140
TAGTCTAAAA	CACTTACCAC	TAAACGGAAC	TGCACCAGCA	GAAGTTCGTC	AAAAGACTGA	1200
AGTAGGAGGA	CCACTAGCTA	TCCTAGATTC	ATACTATGGT	AAAGTAACAA	CCATGCCTGA	1260

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TGATGCCAAA TGGCGTTTGG ATCTTATCAA AGAATATTAT GTTCCTTACA TGAGCAATGT      1320
CAATAACTAT CCAAGAGTCT TTATGACACA GGAAGATTTG GACAAGATTG CCCATATCGA      1380
AGCAGATATG AATGACTATA TCTACCGTAA ACGTGCTGAA TGGATTGTAA ATGGCAATAT      1440
TGATACTGAG TGGGATGATT ACAAGAAAGA ACTTGAAAAA TACGGACTTT CTGATTACCT      1500
CGCTATTAAA CAAAATACT ACGACCAATA CCAAGCAAAC AAAAAC                        1546

```

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Gly Ser Lys Asn Thr Ala Ser Ser Pro Asp Tyr Lys Leu Glu Gly Val
1          5          10          15
Thr Phe Pro Leu Gln Glu Lys Lys Thr Leu Lys Phe Met Thr Ala Ser
20          25          30
Ser Pro Leu Ser Pro Lys Asp Pro Asn Glu Lys Leu Ile Leu Gln Arg
35          40          45
Leu Glu Lys Glu Thr Gly Val His Ile Asp Trp Thr Asn Tyr Gln Ser
50          55          60
Asp Phe Ala Glu Lys Arg Asn Leu Asp Ile Ser Ser Gly Asp Leu Pro
65          70          75          80
Asp Ala Ile His Asn Asp Gly Ala Ser Asp Val Asp Leu Met Asn Trp
85          90          95
Ala Lys Lys Gly Val Ile Ile Pro Val Glu Asp Leu Ile Asp Lys Tyr
100         105         110
Met Pro Asn Leu Lys Lys Ile Leu Asp Glu Lys Pro Glu Tyr Lys Ala
115         120         125
Leu Met Thr Ala Pro Asp Gly His Ile Tyr Ser Phe Pro Trp Ile Glu
130         135         140
Glu Leu Gly Asp Gly Lys Glu Ser Ile His Ser Val Asn Asp Met Ala
145         150         155         160
Trp Ile Asn Lys Asp Trp Leu Lys Lys Leu Gly Leu Glu Met Pro Lys
165         170         175
Thr Thr Asp Asp Leu Ile Lys Val Leu Glu Ala Phe Lys Asn Gly Asp
180         185         190
Pro Asn Gly Asn Gly Glu Ala Asp Glu Ile Pro Phe Ser Phe Ile Ser
195         200         205
Gly Asn Gly Asn Glu Asp Phe Lys Phe Leu Phe Ala Ala Phe Gly Ile

```

210					215					220					
Gly 225	Asp	Asn	Asp	Asp	His 230	Leu	Val	Val	Gly	Asn 235	Asp	Gly	Lys	Val	Asp 240
Phe	Thr	Ala	Asp	Asn 245	Asp	Asn	Tyr	Lys	Glu 250	Gly	Val	Lys	Phe	Ile 255	Arg
Gln	Leu	Gln	Glu 260	Lys	Gly	Leu	Ile	Asp 265	Lys	Glu	Ala	Phe	Glu 270	His	Asp
Trp	Asn	Ser 275	Tyr	Ile	Ala	Lys	Gly 280	His	Asp	Gln	Lys	Phe 285	Gly	Val	Tyr
Phe	Thr 290	Trp	Asp	Lys	Asn	Asn 295	Val	Thr	Gly	Ser	Asn 300	Glu	Ser	Tyr	Asp
Val 305	Leu	Pro	Val	Leu	Ala 310	Gly	Pro	Ser	Gly	Gln 315	Lys	His	Val	Ala	Arg 320
Thr	Asn	Gly	Met	Gly 325	Phe	Ala	Arg	Asp	Lys 330	Met	Val	Ile	Thr	Ser 335	Val
Asn	Lys	Asn	Leu 340	Glu	Leu	Thr	Ala	Lys 345	Trp	Ile	Asp	Ala	Gln 350	Tyr	Ala
Pro	Leu	Gln 355	Ser	Val	Gln	Asn	Asn 360	Trp	Gly	Thr	Tyr	Gly 365	Asp	Asp	Lys
Gln 370	Gln	Asn	Ile	Phe	Glu	Leu 375	Asp	Gln	Ala	Ser	Asn 380	Ser	Leu	Lys	His
Leu 385	Pro	Leu	Asn	Gly	Thr 390	Ala	Pro	Ala	Glu	Leu 395	Arg	Gln	Lys	Thr	Glu 400
Val	Gly	Gly	Pro	Leu 405	Ala	Ile	Leu	Asp	Ser 410	Tyr	Tyr	Gly	Lys	Val 415	Thr
Thr	Met	Pro	Asp 420	Asp	Ala	Lys	Trp	Arg 425	Leu	Asp	Leu	Ile	Lys 430	Glu	Tyr
Tyr	Val	Pro	Tyr 435	Met	Ser	Asn	Val 440	Asn	Asn	Tyr	Pro	Arg 445	Val	Phe	Met
Thr 450	Gln	Glu	Asp	Leu	Asp	Lys 455	Ile	Ala	His	Ile	Glu 460	Ala	Asp	Met	Asn
Asp 465	Tyr	Ile	Tyr	Arg	Lys 470	Arg	Ala	Glu	Trp	Ile 475	Val	Asn	Gly	Asn 480	Ile
Asp	Thr	Glu	Trp	Asp 485	Asp	Tyr	Lys	Lys	Glu 490	Leu	Glu	Lys	Tyr	Gly 495	Leu
Ser	Asp	Tyr	Leu 500	Ala	Ile	Lys	Gln	Lys 505	Tyr	Tyr	Asp	Gln	Tyr 510	Gln	Ala
Asn	Lys	Asn 515													

## (2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 895 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TAGTACAAAC TCAAGCACTA GTCAGACAGA GACCAGTAGC TCTGCTCCAA CAGAGGTAAC	60
CATTAAAAGT TCACTGGACG AGGTCAAAC TCCAAAGTT CCTGAAAAGA TTGTGACCTT	120
TGACCTCGGC GCTGCGGATA CTATTCGCGC TTTAGGATTT GAAAAAATA TCGTCGGAAT	180
GCCTACAAAA ACTGTTCCGA CTTATCTAAA AGACCTAGTG GGAAGTGTCA AAAATGTTGG	240
TTCTATGAAA GAACCTGATT TAGAAGCTAT CGCCGCCCTT GAGCCTGATT TGATTATCGC	300
TTGCCACGT ACACAAAAT TCGTAGACAA ATTCAAAGAA ATCGCCCCAA CCGTTCTCTT	360
CCAAGCAAGC AAGGACGACT ACTGGACTTC TACCAAGGCT AATATCGAAT CCTTAGCAAG	420
TGCCTTCGGC GAAACTGGTA CACAGAAAGC CAAGGAAGAA TTGACCAAGC TAGACAAGAG	480
CATCCAAGAA GTCGCTACTA AAAATGAAAG CTCTGACAAA AAAGCCCTTG CGATCCTCCT	540
TAATGAAGGA AAAATGGCAG CCTTTGGTGC CAAATCTCGT TTCTCTTTCT TGTACCAAAC	600
CTTGAAATTC AAACCAACTG ATACAAAATT TGAAGACTCA CGCCACGGAC AAGAAGTCAG	660
CTTTGAAAGT GTCAAAGAAA TCAACCCTGA CATCCTCTTT GTCATCAACC GTACCCTTGC	720
CATCGGTGGG GACAACTCTA GCAACGACGG TGTCCTAGAA AATGCCCTTA TCGCTGAAAC	780
ACCTGCTGCT AAAAATGGTA AGATTATCCA ACTAACACCA GACCTCTGGT ATCTAAGCGG	840
AGGCGGACTT GAATCAACAA AACTCATGAT TGAAGACATA CAAAAGCTT TGAAA	895

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 298 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Thr Asn Ser Ser Thr Ser Gln Thr Glu Thr Ser Ser Ser Ala Pro	1 5 10 15
Thr Glu Val Thr Ile Lys Ser Ser Leu Asp Glu Val Lys Leu Ser Lys	20 25 30
Val Pro Glu Lys Ile Val Thr Phe Asp Leu Gly Ala Ala Asp Thr Ile	35 40 45
Arg Ala Leu Gly Phe Glu Lys Asn Ile Val Gly Met Pro Thr Lys Thr	50 55 60
Val Pro Thr Tyr Leu Lys Asp Leu Val Gly Thr Val Lys Asn Val Gly	65 70 75 80

Ser Met Lys Glu Pro Asp Leu Glu Ala Ile Ala Ala Leu Glu Pro Asp  
 85 90 95  
 Leu Ile Ile Ala Ser Pro Arg Thr Gln Lys Phe Val Asp Lys Phe Lys  
 100 105 110  
 Glu Ile Ala Pro Thr Val Leu Phe Gln Ala Ser Lys Asp Asp Tyr Trp  
 115 120 125  
 Thr Ser Thr Lys Ala Asn Ile Glu Ser Leu Ala Ser Ala Phe Gly Glu  
 130 135 140  
 Thr Gly Thr Gln Lys Ala Lys Glu Glu Leu Thr Lys Leu Asp Lys Ser  
 145 150 155 160  
 Ile Gln Glu Val Ala Thr Lys Asn Glu Ser Ser Asp Lys Lys Ala Leu  
 165 170 175  
 Ala Ile Leu Leu Asn Glu Gly Lys Met Ala Ala Phe Gly Ala Lys Ser  
 180 185 190  
 Arg Phe Ser Phe Leu Tyr Gln Thr Leu Lys Phe Lys Pro Thr Asp Thr  
 195 200 205  
 Lys Phe Glu Asp Ser Arg His Gly Gln Glu Val Ser Phe Glu Ser Val  
 210 215 220  
 Lys Glu Ile Asn Pro Asp Ile Leu Phe Val Ile Asn Arg Thr Leu Ala  
 225 230 235 240  
 Ile Gly Gly Asp Asn Ser Ser Asn Asp Gly Val Leu Glu Asn Ala Leu  
 245 250 255  
 Ile Ala Glu Thr Pro Ala Ala Lys Asn Gly Lys Ile Ile Gln Leu Thr  
 260 265 270  
 Pro Asp Leu Trp Tyr Leu Ser Gly Gly Gly Leu Glu Ser Thr Lys Leu  
 275 280 285  
 Met Ile Glu Asp Ile Gln Lys Ala Leu Lys  
 290 295

## (2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1261 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TGGCAATTCT GCGGAAGTA AAGATGCTGC CAAATCAGGT GGTGACGGTG CAAAAACAGA	60
AATCACTTGG TGGGCATTCC CAGTATTTAC CCAAGAAAAA ACTGGTGACG GTGTTGGAAC	120
TTATGAAAAA TCAATCATCG AAGCGTTTGA AAAAGCAAAC CCAGATATAA AAGTGAAATT	180
GGAAACCATC GACTTCAAGT CAGGTCCTGA AAAAATCACA ACAGCCATCG AAGCAGGAAC	240
AGCTCCAGAC GTACTCTTTG ATGCACCAGG ACGTATCATC CAATACGGTA AAAACGGTAA	300

```

ATTGGCTGAG TTGAATGACC TCTTCACAGA TGAATTTGTT AAAGATGTCA ACAATGAAAA 360
CATCGTACAA GCAAGTAAAG CTGGAGACAA GGCTTATATG TATCCGATTA GTTCTGCCCC 420
ATTCTACATG GCAATGAACA AGAAAATGTT AGAAGATGCT GGAGTAGCAA ACCTTGTAAG 480
AGAAGGTTGG ACAACTGATG ATTTTGAAAA AGTATTGAAA GCACTTAAAG ACAAGGGTTA 540
CACACCAGGT TCATTGTTCA GTTCTGGTCA AGGGGGAGAC CAAGGAACAC GTGCCTTTAT 600
CTCTAACCTT TATAGCGGTT CTGTAACAGA TGAAAAAGTT AGCAAATATA CAACTGATGA 660
TCCTAAATTC GTCAAAGGTC TTGAAAAAGC AACTAGCTGG ATTAAGACA ATTTGATCAA 720
TAATGGTTCA CAATTTGACG GTGGGGCAGA TATCCAAAAC TTTGCCAACG GTCAAACATC 780
TTACACAATC CTTTGGGCAC CAGCTCAAAA TGGTATCCAA GCTAAACTTT TAGAAGCAAG 840
TAAGGTAGAA GTGGTAGAAG TACCATTCCC ATCAGACGAA GGTAAGCCAG CTCTTGAGTA 900
CCTTGTAAC GGGTTTGCAG TATTCAACAA TAAAGACGAC AAGAAAGTCG CTGCATCTAA 960
GAAATTCATC CAGTTTATCG CAGATGACAA GGAGTGGGGA CCTAAAGACG TAGTTCGTAC 1020
AGGTGCTTTC CCAGTCCGTA CTTTATTGTTG AAAACTTTAT GAAGACAAAC GCATGGAAAC 1080
AATCAGCGGC TGGACTCAAT ACTACTCACC ATACTACAAC ACTATTGATG GATTGCTGA 1140
AATGAGAACA CTTTGGTTCC CAATGTTGCA ATCTGTATCA AATGGTGACG AAAAACCAGC 1200
AGATGCTTTG AAAGCCTTCA CTGAAAAAGC GAACGAAACA ATCAAAAAAG CTATGAAACA 1260
A 1261

```

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Gly Asn Ser Gly Gly Ser Lys Asp Ala Ala Lys Ser Gly Gly Asp Gly
1           5           10           15
Ala Lys Thr Glu Ile Thr Trp Trp Ala Phe Pro Val Phe Thr Gln Glu
20           25           30
Lys Thr Gly Asp Gly Val Gly Thr Tyr Glu Lys Ser Ile Ile Glu Ala
35           40           45
Phe Glu Lys Ala Asn Pro Asp Ile Lys Val Lys Leu Glu Thr Ile Asp
50           55           60
Phe Lys Ser Gly Pro Glu Lys Ile Thr Thr Ala Ile Glu Ala Gly Thr
65           70           75           80
Ala Pro Asp Val Leu Phe Asp Ala Pro Gly Arg Ile Ile Gln Tyr Gly

```

85					90					95					
Lys	Asn	Gly	Lys	Leu	Ala	Glu	Leu	Asn	Asp	Leu	Phe	Thr	Asp	Glu	Phe
			100					105					110		
Val	Lys	Asp	Val	Asn	Asn	Glu	Asn	Ile	Val	Gln	Ala	Ser	Lys	Ala	Gly
		115					120					125			
Asp	Lys	Ala	Tyr	Met	Tyr	Pro	Ile	Ser	Ser	Ala	Pro	Phe	Tyr	Met	Ala
	130					135					140				
Met	Asn	Lys	Lys	Met	Leu	Glu	Asp	Ala	Gly	Val	Ala	Asn	Leu	Val	Lys
	145				150					155					160
Glu	Gly	Trp	Thr	Thr	Asp	Asp	Phe	Glu	Lys	Val	Leu	Lys	Ala	Leu	Lys
				165					170					175	
Asp	Lys	Gly	Tyr	Thr	Pro	Gly	Ser	Leu	Phe	Ser	Ser	Gly	Gln	Gly	Gly
			180					185					190		
Asp	Gln	Gly	Thr	Arg	Ala	Phe	Ile	Ser	Asn	Leu	Tyr	Ser	Gly	Ser	Val
		195					200					205			
Thr	Asp	Glu	Lys	Val	Ser	Lys	Tyr	Thr	Thr	Asp	Asp	Pro	Lys	Phe	Val
	210					215					220				
Lys	Gly	Leu	Glu	Lys	Ala	Thr	Ser	Trp	Ile	Lys	Asp	Asn	Leu	Ile	Asn
	225				230					235					240
Asn	Gly	Ser	Gln	Phe	Asp	Gly	Gly	Ala	Asp	Ile	Gln	Asn	Phe	Ala	Asn
				245					250					255	
Gly	Gln	Thr	Ser	Tyr	Thr	Ile	Leu	Trp	Ala	Pro	Ala	Gln	Asn	Gly	Ile
			260					265					270		
Gln	Ala	Lys	Leu	Leu	Glu	Ala	Ser	Lys	Val	Glu	Val	Val	Glu	Val	Pro
		275					280					285			
Phe	Pro	Ser	Asp	Glu	Gly	Lys	Pro	Ala	Leu	Glu	Tyr	Leu	Val	Asn	Gly
	290					295					300				
Phe	Ala	Val	Phe	Asn	Asn	Lys	Asp	Asp	Lys	Lys	Val	Ala	Ala	Ser	Lys
	305				310					315					320
Lys	Phe	Ile	Gln	Phe	Ile	Ala	Asp	Asp	Lys	Glu	Trp	Gly	Pro	Lys	Asp
				325					330					335	
Val	Val	Arg	Thr	Gly	Ala	Phe	Pro	Val	Arg	Thr	Ser	Phe	Gly	Lys	Leu
			340					345					350		
Tyr	Glu	Asp	Lys	Arg	Met	Glu	Thr	Ile	Ser	Gly	Trp	Thr	Gln	Tyr	Tyr
		355				360						365			
Ser	Pro	Tyr	Tyr	Asn	Thr	Ile	Asp	Gly	Phe	Ala	Glu	Met	Arg	Thr	Leu
	370					375					380				
Trp	Phe	Pro	Met	Leu	Gln	Ser	Val	Ser	Asn	Gly	Asp	Glu	Lys	Pro	Ala
	385				390					395					400
Asp	Ala	Leu	Lys	Ala	Phe	Thr	Glu	Lys	Ala	Asn	Glu	Thr	Ile	Lys	Lys
				405					410					415	
Ala	Met	Lys	Gln												
			420												

## (2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 658 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

TTCACAAGAA AAAACAAAAA ATGAAGATGG AGAAACTAAG ACAGAACAGA CAGCCAAAGC      60
TGATGGAACA GTCGGTAGTA AGTCTCAAGG AGCTGCCCAG AAGAAAGCAG AAGTGGTCAA      120
TAAAGGTGAT TACTACAGCA TTCAAGGGAA ATACGATGAA ATCATCGTAG CCAACAAACA      180
CTATCCATTG TCTAAAGACT ATAATCCAGG GGAAAATCCA ACAGCCAAGG CAGAGTTGGT      240
CAAACATCATC AAAGCGATGC AAGAGGCAGG TTTCCCTATT AGTGATCATT ACAGTGGTTT      300
TAGAAGTTAT GAAACTCAGA CCAAGCTCTA TCAAGATTAT GTCAACCAAG ATGGAAAGGC      360
AGCAGCTGAC CGTACTCTG CCCGTCCTGG CTATAGCGAA CACCAGACAG GCTTGGCCTT      420
TGATGTGATT GGGACTGATG GTGATTTGGT GACAGAAGAA AAAGCAGCCC AATGGCTCTT      480
GGATCATGCA GCTGATTATG GCTTTGTTGT CCGTTATCTC AAAGGCAAGG AAAAGGAAAC      540
AGGCTATATG GCTGAAGAAT GGCACCTGCG TTATGTAGGA AAAGAAGCTA AAGAAATTGC      600
TGCAAGTGGT CTCAGTTTGG AAGAATACTA TGGCTTTGAA GCGGAGACT ACGTCGAT      658

```

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 219 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Ser Gln Glu Lys Thr Lys Asn Glu Asp Gly Glu Thr Lys Thr Glu Gln
1          5          10
Thr Ala Lys Ala Asp Gly Thr Val Gly Ser Lys Ser Gln Gly Ala Ala
20        25        30
Gln Lys Lys Ala Glu Val Val Asn Lys Gly Asp Tyr Tyr Ser Ile Gln
35        40        45
Gly Lys Tyr Asp Glu Ile Ile Val Ala Asn Lys His Tyr Pro Leu Ser
50        55        60
Lys Asp Tyr Asn Pro Gly Glu Asn Pro Thr Ala Lys Ala Glu Leu Val
65        70        75        80
Lys Leu Ile Lys Ala Met Gln Glu Ala Gly Phe Pro Ile Ser Asp His

```

				85						90					95				
Tyr	Ser	Gly	Phe	Arg	Ser	Tyr	Glu	Thr	Gln	Thr	Lys	Leu	Tyr	Gln	Asp				
			100					105					110						
Tyr	Val	Asn	Gln	Asp	Gly	Lys	Ala	Ala	Ala	Asp	Arg	Tyr	Ser	Ala	Arg				
		115					120					125							
Pro	Gly	Tyr	Ser	Glu	His	Gln	Thr	Gly	Leu	Ala	Phe	Asp	Val	Ile	Gly				
	130					135					140								
Thr	Asp	Gly	Asp	Leu	Val	Thr	Glu	Glu	Lys	Ala	Ala	Gln	Trp	Leu	Leu				
	145				150					155					160				
Asp	His	Ala	Ala	Asp	Tyr	Gly	Phe	Val	Val	Arg	Tyr	Leu	Lys	Gly	Lys				
				165					170					175					
Glu	Lys	Glu	Thr	Gly	Tyr	Met	Ala	Glu	Glu	Trp	His	Leu	Arg	Tyr	Val				
			180					185					190						
Gly	Lys	Glu	Ala	Lys	Glu	Ile	Ala	Ala	Ser	Gly	Leu	Ser	Leu	Glu	Glu				
		195					200					205							
Tyr	Tyr	Gly	Phe	Glu	Gly	Gly	Asp	Tyr	Val	Asp									
	210					215													

## (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 790 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GAAAGGTCTG TGGTCAAATA ATCTTACCTG CGGTTATGAT GAAAAAATAA TCTTGGA	60
TATAATATA AAAATACCTG AAGAAAAAAT ATCAGTTATT ATGGGTCAA ATGGTTGTGG	120
GAAATCAACA CTCATTAAAA CCTTGTCTCG ACTTATAAAG CCATTAGAGG GAGAAGTATT	180
GCTTGATAAT AAATCAATTA ATTCTTATAA AGAAAAAGAT TTAGCAAAAC ACATAGCTAT	240
ATTACCTCAA TCTCCAATAA TCCCTGAATC AATAACAGTA GCTGATCTTG TAAGCCGTGG	300
TCGTTTCCCC TACAGAAAGC CTTTAAAGAG TCTTGGA	360
GATGACCTTG AAATAATAAA	
CAGATCAATG GTTAAGGCCA ATGTTGAAGA TCTAGCAAAT AACCTAGTTG AAGAACTTTC	420
TGGGGGTCAA AGGCAAAGAG TATGGATAGC TCTAGCCCTA GCCCAAGATA CAAGTATCCT	480
ACTTTTAGAT GAGCCAACTA CTTACTTGGA TATCTCATAT CAAATAGAAC TATTAGACCT	540
CTTGACTGAT CTAAACCAAA AATATAAGAC AACCATTTCG ATGATTTTGC ACGATATAAA	600
TCTAACAGCA AGATACGCTG ATTACCTATT TGCAATTAAA GAAGGTAAAC TTGTTGCAGA	660
GGGAAAGCCT GAAGATATAC TAAATGATAA ACTAGTTAAA GATATCTTTA ATCTTGAAGC	720
AAAAATTATA CGTGACCCTA TTTCCAATTC GCCTCTAATG ATTCCTATTG GCAAGCACCA	780

TGTTAACTCT

790

## (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 262 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Gly Leu Trp Ser Asn Asn Leu Thr Cys Gly Tyr Asp Glu Lys Ile  
 1 5 10 15  
 Ile Leu Glu Asn Ile Asn Ile Lys Ile Pro Glu Glu Lys Ile Ser Val  
 20 25 30  
 Ile Ile Gly Ser Asn Gly Cys Gly Lys Ser Thr Leu Ile Lys Thr Leu  
 35 40 45  
 Ser Arg Leu Ile Lys Pro Leu Glu Gly Glu Val Leu Leu Asp Asn Lys  
 50 55 60  
 Ser Ile Asn Ser Tyr Lys Glu Lys Asp Leu Ala Lys His Ile Ala Ile  
 65 70 75 80  
 Leu Pro Gln Ser Pro Ile Ile Pro Glu Ser Ile Thr Val Ala Asp Leu  
 85 90 95  
 Val Ser Arg Gly Arg Phe Pro Tyr Arg Lys Pro Phe Lys Ser Leu Gly  
 100 105 110  
 Lys Asp Asp Leu Glu Ile Ile Asn Arg Ser Met Val Lys Ala Asn Val  
 115 120 125  
 Glu Asp Leu Ala Asn Asn Leu Val Glu Glu Leu Ser Gly Gly Gln Arg  
 130 135 140  
 Gln Arg Val Trp Ile Ala Leu Ala Leu Ala Gln Asp Thr Ser Ile Leu  
 145 150 155 160  
 Leu Leu Asp Glu Pro Thr Thr Tyr Leu Asp Ile Ser Tyr Gln Ile Glu  
 165 170 175  
 Leu Leu Asp Leu Leu Thr Asp Leu Asn Gln Lys Tyr Lys Thr Thr Ile  
 180 185 190  
 Cys Met Ile Leu His Asp Ile Asn Leu Thr Ala Arg Tyr Ala Asp Tyr  
 195 200 205  
 Leu Phe Ala Ile Lys Glu Gly Lys Leu Val Ala Glu Gly Lys Pro Glu  
 210 215 220  
 Asp Ile Leu Asn Asp Lys Leu Val Lys Asp Ile Phe Asn Leu Glu Ala  
 225 230 235 240  
 Lys Ile Ile Arg Asp Pro Ile Ser Asn Ser Pro Leu Met Ile Pro Ile  
 245 250 255  
 Gly Lys His His Val Ser

260

## (2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 781 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

AAACTCAGAA AAGAAAGCAG ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG      60
CGGTTCTGAA GAAAAACGTT GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACGGAATTAC      120
CTTGGAATTT ACAGAGTTCA CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA      180
AGTAGATTTG AACGCTTTCC AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG      240
AAAAGACCTT GTAGCGATTG CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT      300
GAATGGAAGT GCCAACAAGT AACTTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCGC      360
TGTACCGAAT GACGCTACAA ACGAAAGCCG TGCGCTTTAT TTGCTTCAAT CAGCTGGCTT      420
GATTAAATTG GATGTTTCTG GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC      480
AAAGAACTTG AAAATCACTG AATTGGACGC TAGCCAAACA GTCGTTTCAT TGTCATCAGT      540
TGACGCTGCC GTTGTAACA ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC      600
ACTTTTCAAA GAACAAGCTG ATGAAAACTC AAAACAATGG TACAACATCA TTGTTGCAAA      660
AAAAGATTGG GAAACATCAC CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA      720
CACAGATGAC GTGAAAAAAG TTATCGAAGA ATCATCAGAT GGTTCGGATC AACCAGTTTG      780
G

```

## (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 260 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Asn Ser Glu Lys Lys Ala Asp Asn Ala Thr Thr Ile Lys Ile Ala Thr
1           5           10          15
Val Asn Arg Ser Gly Ser Glu Glu Lys Arg Trp Asp Lys Ile Gln Glu
20          25          30
Leu Val Lys Lys Asp Gly Ile Thr Leu Glu Phe Thr Glu Phe Thr Asp
35          40          45

```

Tyr Ser Gln Pro Asn Lys Ala Thr Ala Asp Gly Glu Val Asp Leu Asn  
 50 55 60  
 Ala Phe Gln His Tyr Asn Phe Leu Asn Asn Trp Asn Lys Glu Asn Gly  
 65 70 75 80  
 Lys Asp Leu Val Ala Ile Ala Asp Thr Tyr Ile Ser Pro Ile Arg Leu  
 85 90 95  
 Tyr Ser Gly Leu Asn Gly Ser Ala Asn Lys Tyr Thr Lys Val Glu Asp  
 100 105 110  
 Ile Pro Ala Asn Gly Glu Ile Ala Val Pro Asn Asp Ala Thr Asn Glu  
 115 120 125  
 Ser Arg Ala Leu Tyr Leu Leu Gln Ser Ala Gly Leu Ile Lys Leu Asp  
 130 135 140  
 Val Ser Gly Thr Ala Leu Ala Thr Val Ala Asn Ile Lys Glu Asn Pro  
 145 150 155 160  
 Lys Asn Leu Lys Ile Thr Glu Leu Asp Ala Ser Gln Thr Ala Arg Ser  
 165 170 175  
 Leu Ser Ser Val Asp Ala Ala Val Val Asn Asn Thr Phe Val Thr Glu  
 180 185 190  
 Ala Lys Leu Asp Tyr Lys Lys Ser Leu Phe Lys Glu Gln Ala Asp Glu  
 195 200 205  
 Asn Ser Lys Gln Trp Tyr Asn Ile Ile Val Ala Lys Lys Asp Trp Glu  
 210 215 220  
 Thr Ser Pro Lys Ala Asp Ala Ile Lys Lys Val Ile Ala Ala Tyr His  
 225 230 235 240  
 Thr Asp Asp Val Lys Lys Val Ile Glu Glu Ser Ser Asp Gly Leu Asp  
 245 250 255  
 Gln Pro Val Trp  
 260

## (2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 640 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TTCGAAAGGG TCAGAAGGTG CAGACCTTAT CAGCATGAAA GGGGATGTCA TTACAGAACA	60
TCAATTTTAT GAGCAAGTGA AAAGCAACCC TTCAGCCCAA CAAGTCTTGT TAAATATGAC	120
CATCCAAAAA GTTTTGTAAA AACAATATGG CTCAGAGCTT GATGATAAAG AGGTTGATGA	180
TACTATTGCC GAAGAAAAAA AACAATATGG CGAAAACTAC CAACGTGTCT TGTCACAAGC	240
AGGTATGACT CTTGAAACAC GTAAAGCTCA AATTCGTACA AGTAAATTAG TTGAGTTGGC	300

```

AGTTAAGAAG GTAGCAGAAG CTGAATTGAC AGATGAAGCC TATAAGAAAG CCTTTGATGA      360
GTACACTCCA GATGTAACGG CTCAAATCAT CCGTCTTAAT AATGAAGATA AGGCCAAAGA      420
AGTTCTCGAA AAAGCCAAGG CAGAAGGTGC TGATTTTGCT CAATTAGCCA AAGATAATTC      480
AACTGATGAA AAAACAAAAG AAAATGGTGG AGAAATTACC TTTGATTCTG CTTCAACAGA      540
AGTACCTGGA GCAAGTCCAA AAAAGCCGCT TTTCGCTTTT AGATGTGGGA TGGTGTTTCT      600
GGATGTGGAT TACAGCAACT GGGGCACACC AAGCCTACAG                               640

```

## (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 213 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

Ser Lys Gly Ser Glu Gly Ala Asp Leu Ile Ser Met Lys Gly Asp Val
1      5      10      15
Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys Ser Asn Pro Ser Ala
20     25     30
Gln Gln Val Leu Leu Asn Met Thr Ile Gln Lys Val Phe Glu Lys Gln
35     40     45
Tyr Gly Ser Glu Leu Asp Asp Lys Glu Val Asp Asp Thr Ile Ala Glu
50     55     60
Glu Lys Lys Gln Tyr Gly Glu Asn Tyr Gln Arg Val Leu Ser Gln Ala
65     70     75     80
Gly Met Thr Leu Glu Thr Arg Lys Ala Gln Ile Arg Thr Ser Lys Leu
85     90     95
Val Glu Leu Ala Val Lys Lys Val Ala Glu Ala Glu Leu Thr Asp Glu
100    105    110
Ala Tyr Lys Lys Ala Phe Asp Glu Tyr Thr Pro Asp Val Thr Ala Gln
115    120    125
Ile Ile Arg Leu Asn Asn Glu Asp Lys Ala Lys Glu Val Leu Glu Lys
130    135    140
Ala Lys Ala Glu Gly Ala Asp Phe Ala Gln Leu Ala Lys Asp Asn Ser
145    150    155    160
Thr Asp Glu Lys Thr Lys Glu Asn Gly Gly Glu Ile Thr Phe Asp Ser
165    170    175
Ala Ser Thr Glu Val Pro Gly Ala Ser Pro Lys Lys Pro Leu Phe Ala
180    185    190
Phe Arg Cys Gly Met Val Phe Leu Asp Val Asp Tyr Ser Asn Trp Gly
195    200    205

```

Thr Pro Ser Leu Gln  
210

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 631 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

GGGGATGGCA GCTTTTAAAA ATCCTAACAA TCAATACAAA GCTATTACAA TTGCTCAAAC      60
TCTAGGTGAT GATGCTTCTT CAGAGGAATT GGCTGGTAGA TATGGTTCTG CTGTTTCAGTG      120
TACAGAAAGTG ACTGCCTCAA ACCTTTCAAC AGTTAAAACT AAAGCTACGG TTGTAGAAAA      180
ACCACTGAAA GATTTTtagag CGTCTACGTC TGATCAGTCT GGTGGGTGG AATCTAATGG      240
TAAATGGTAT TTCTATGAGT CTGGTGATGT GAAGACAGGT TGGGTGAAAA CAGATGGTAA      300
ATGGTACTAT TTGAATGACT TAGGTGTCAT GCAGACTGGA TTTGTAAAAT TTTCTGGTAG      360
CTGGTATTAC TTGAGCAATT CAGGTGCTAT GTTACAGGC TGGGGAACAG ATGGTAGCAG      420
ATGGTTCCTAC TTTGACGGCT CAGGAGCTAT GAAGACAGGC TGGTACAAGG AAAATGGCAC      480
TTGGTATTAC CTTGACGAAG CAGGTATCAT GAAGACAGGT TGGTTTAAAG TCGGACCACA      540
CTGGTACTAT GCCTACGGTT CAGGAGCTTT GGCTGTGAGC ACAACAACAC CAGATGGTTA      600
CCGTGTAAAT GGTAATGGTG AATGGGTAAA C      631
  
```

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 210 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Gly Met Ala Ala Phe Lys Asn Pro Asn Asn Gln Tyr Lys Ala Ile Thr
1           5           10           15
Ile Ala Gln Thr Leu Gly Asp Asp Ala Ser Ser Glu Glu Leu Ala Gly
20          25          30
Arg Tyr Gly Ser Ala Val Gln Cys Thr Glu Val Thr Ala Ser Asn Leu
35          40          45
Ser Thr Val Lys Thr Lys Ala Thr Val Val Glu Lys Pro Leu Lys Asp
50          55          60
Phe Arg Ala Ser Thr Ser Asp Gln Ser Gly Trp Val Glu Ser Asn Gly
65          70          75          80
  
```

[illegible]

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

AGACGAGCAA	AAAATTAAGC	AAGCAGAAGC	GGAAGTTGAG	AGTAAACAAG	CTGAGGCTAC	60
AAGGTTAAAA	AAAATCAAGA	CAGATCGTGA	AGAAGCAGAA	GAAGAAGCTA	AACGAAGAGC	120
AGATGCTAAA	GAGCAAGGTA	AACCAAAGGG	GCGGGCAAAA	CGAGGAGTTC	CTGGAGAGCT	180
AGCAACACCT	GATAAAAAAG	AAAATGATGC	GAAGTCTTCA	GATTCTAGCG	TAGGTGAAGA	240
AACTCTTCCA	AGCCCATCCC	TGAAACCAGA	AAAAAAGGTA	GCAGAAGCTG	AGAAGAAGGT	300
TGAAGAAGCT	AAGAAAAAAG	CCGAGGATCA	AAAAGAAGAA	GATCGCCGTA	ACTACCCAAC	360
CAATACTTAC	AAAACGCTTG	AACTTGAAAT	TGCTGAGTCC	GATGTGGAAG	TTAAAAAAGC	420
GGAGCTTGAA	CTAGTAAAAG	AGGAAGCTAA	GGAACCTCGA	AACGAGGAAA	AAGTTAAGCA	480
AGCAAAAGCG	GAAGTTGAGA	GTAAAAAAGC	TGAGGCTACA	AGGTTAGAAA	AAATCAAGAC	540
AGATCGTAAA	AAAGCAGAAG	AAGAAGCTAA	ACGAAAAGCA	GCAGAAGAAG	ATAAAGTTAA	600
AGAAAAACCA	GCTGAACAAC	CACAACCAGC	GCCGGCTCCA	AAAGCAGAAA	AACCAGCTCC	660
AGCTCCAAAA	CCAGAGAATC	CAGCTGAACA	ACCAAAAAGCA	GAAAAACCAG	CTGATCAACA	720

AGCTGAAGAA GACTATGCTC GTAGATCAGA AGAAGAATAT AATCGCTTGA CTCAACAGCA	780
ACCGCCAAAA ACTGAAAAAC CAGCACAACC ATCTACTCCA AAAACAGGCT GGAAACAAGA	840
AAACGGTATG TGGTACTTCT ACAATACTGA TGGTTCAATG GCGACAGGAT GGCTCCAAAA	900
CAATGGCTCA TGGTACTACC TCAACAGCAA TGGCGCTATG GCGACAGGAT GGCTCCAAAA	960
CAATGGTTCA TGGTACTATC TAAACGCTAA TGGTTCAATG GCAACAGGAT GGCTCCAAAA	1020
CAATGGTTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA	1080
CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA	1140
CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTGATATG GCGACAGGTT GGGTGAAAGA	1200
TGGAGATACC TGGTACTATC TTGAAGCATC AGGTGCTATG AAAGCAAGCC AATGGTTCAA	1260
AGTATCAGAT AAATGGTACT ATGTCAATGG CTCAGGTGCC CTTGCAGTCA ACACAACTGT	1320
AGATGGCTAT GGAGTCAATG CCAATGGTGA ATGGGTAAAC	1360

## (2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 453 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Asp	Glu	Gln	Lys	Ile	Lys	Gln	Ala	Glu	Ala	Glu	Val	Glu	Ser	Lys	Gln	1	5	10	15
Ala	Glu	Ala	Thr	Arg	Leu	Lys	Lys	Ile	Lys	Thr	Asp	Arg	Glu	Glu	Ala	20	25	30	
Glu	Glu	Glu	Ala	Lys	Arg	Arg	Ala	Asp	Ala	Lys	Glu	Gln	Gly	Lys	Pro	35	40	45	
Lys	Gly	Arg	Ala	Lys	Arg	Gly	Val	Pro	Gly	Glu	Leu	Ala	Thr	Pro	Asp	50	55	60	
Lys	Lys	Glu	Asn	Asp	Ala	Lys	Ser	Ser	Asp	Ser	Ser	Val	Gly	Glu	Glu	65	70	75	80
Thr	Leu	Pro	Ser	Pro	Ser	Leu	Lys	Pro	Glu	Lys	Lys	Val	Ala	Glu	Ala	85	90	95	
Glu	Lys	Lys	Val	Glu	Glu	Ala	Lys	Lys	Lys	Ala	Glu	Asp	Gln	Lys	Glu	100	105	110	
Glu	Asp	Arg	Arg	Asn	Tyr	Pro	Thr	Asn	Thr	Tyr	Lys	Thr	Leu	Glu	Leu	115	120	125	
Glu	Ile	Ala	Glu	Ser	Asp	Val	Glu	Val	Lys	Lys	Ala	Glu	Leu	Glu	Leu	130	135	140	
Val	Lys	Glu	Glu	Ala	Lys	Glu	Pro	Arg	Asn	Glu	Glu	Lys	Val	Lys	Gln	145	150	155	160

Ala Lys Ala Glu Val Glu Ser Lys Lys Ala Glu Ala Thr Arg Leu Glu  
 165 170 175  
 Lys Ile Lys Thr Asp Arg Lys Lys Ala Glu Glu Glu Ala Lys Arg Lys  
 180 185 190  
 Ala Ala Glu Glu Asp Lys Val Lys Glu Lys Pro Ala Glu Gln Pro Gln  
 195 200 205  
 Pro Ala Pro Ala Pro Lys Ala Glu Lys Pro Ala Pro Ala Pro Lys Pro  
 210 215 220  
 Glu Asn Pro Ala Glu Gln Pro Lys Ala Glu Lys Pro Ala Asp Gln Gln  
 225 230 235 240  
 Ala Glu Glu Asp Tyr Ala Arg Arg Ser Glu Glu Glu Tyr Asn Arg Leu  
 245 250 255  
 Thr Gln Gln Gln Pro Pro Lys Thr Glu Lys Pro Ala Gln Pro Ser Thr  
 260 265 270  
 Pro Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn  
 275 280 285  
 Thr Asp Gly Ser Met Ala Thr Gly Trp Leu Gln Asn Asn Gly Ser Trp  
 290 295 300  
 Tyr Tyr Leu Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Asn  
 305 310 315 320  
 Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser Met Ala Thr Gly  
 325 330 335  
 Trp Leu Gln Asn Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser  
 340 345 350  
 Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn  
 355 360 365  
 Ala Asn Gly Ser Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp  
 370 375 380  
 Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Val Lys Asp  
 385 390 395 400  
 Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser  
 405 410 415  
 Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Ser Gly  
 420 425 430  
 Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Gly Val Asn Ala Asn  
 435 440 445  
 Gly Glu Trp Val Asn  
 450

## (2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 412 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTGTGGTGAG GAAGAACTA AAAAGACTCA AGCAGCACAA CAGCCAAAAC AACAAACGAC	60
TGTACAACAA ATTGCTGTTG GAAAAGATGC TCCAGACTTC ACATTGCAAT CCATGGATGG	120
CAAAGAAGTT AAGTTATCTG ATTTTAAGGG TAAAAGGTT TACTTGAAGT TTTGGGCTTC	180
ATGGTGTGGT CCATGCAAGA AAAGTATGCC AGAGTTGATG GAACTAGCGG CGAAACCAGA	240
TCGTGATTTT GAAATTCTTA CTGTCATTGC ACCAGGAATT CAAGGTGAAA AACTGTTGA	300
GCAATTCCCA CAATGGTTC AGGAACAAGG ATATAAGGAT ATCCCAGTTC TTTATGATAC	360
CAAAGCAACC ACTTCCAAGC TTATCAAATT CGAAGCATTC CTACAGAATA TT	412

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Cys	Gly	Glu	Glu	Glu	Thr	Lys	Lys	Thr	Gln	Ala	Ala	Gln	Gln	Pro	Lys	1	5	10	15
Gln	Gln	Thr	Thr	Val	Gln	Gln	Ile	Ala	Val	Gly	Lys	Asp	Ala	Pro	Asp	20	25	30	
Phe	Thr	Leu	Gln	Ser	Met	Asp	Gly	Lys	Glu	Val	Lys	Leu	Ser	Asp	Phe	35	40	45	
Lys	Gly	Lys	Lys	Val	Tyr	Leu	Lys	Phe	Trp	Ala	Ser	Trp	Cys	Gly	Pro	50	55	60	
Cys	Lys	Lys	Ser	Met	Pro	Glu	Leu	Met	Glu	Leu	Ala	Ala	Lys	Pro	Asp	65	70	75	80
Arg	Asp	Phe	Glu	Ile	Leu	Thr	Val	Ile	Ala	Pro	Gly	Ile	Gln	Gly	Glu	85	90	95	
Lys	Thr	Val	Glu	Gln	Phe	Pro	Gln	Trp	Phe	Gln	Glu	Gln	Gly	Tyr	Lys	100	105	110	
Asp	Ile	Pro	Val	Leu	Tyr	Asp	Thr	Lys	Ala	Thr	Thr	Ser	Lys	Leu	Ile	115	120	125	
Lys	Phe	Glu	Ala	Phe	Leu	Gln	Asn	Ile								130	135		

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1462 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GACTTTTAACTAATAAACTA	TTGAAGAGTTGCACAATCTC	CTTGTCTCTAAGGAAATTTCT	60
TGCAACAGAA	TTGACCCAAGCAACACTTGA	AAATATCAAGTCTCGTGAGG	120
AAGCCCTCAA	TTCATTTGTC	ACCATCGCTGAGGAGCAAGC	180
TCTTGTTCAA	GCTAAAGCCA	TTGATGAAGC	240
tGGAATTGAT	GCTGACAATG	TCCTTTCAGGAATTCCACTT	300
GCTGTTAAGG	ATAACATCTCTACAGACGGT	ATTCTCACAACTGCTGCCTC	360
AAAAATGCTCTACA	ACTATGTAGCCAATCTTTGATGCGACa	gCTgTTGCCA	420
ATGCAAAAAC	CAAGGGCATG	ATTGTCTGTTG	480
GAAAGACCAA	CATGGACGAA	TTTGCTATGGTGGTTCAGG	540
tGAAACTTCA	CACTACGGAG	CAACTAAAA	600
CGCTTGGAAC	CACAGCAAGG	TTCTTGGTGG	660
GTCATCAAGT	GGTTCTGCCG	CAGCTGTAGC	720
CTCAGGACAA	GTTGCTTGT	CACTTGGTTC	780
TGATACTGGT	GGTTCCATCC	GCCAACCTGC	840
TGCCTTCAAC	GGAATCGTTG	GTCTCAAACC	900
AACCTACGGA	ACAGTTTCAC	GTTTCGGTCT	960
CATTGCCTTT	GGTAGCTCAT	TAGACCAGAT	1020
TGGACCTTTT	GCTCCTACTG	TTAAGGAAAA	1080
TGCCCTCTTG	CTCAACGCTA	TTGCCAGCGA	1140
AGATGCTAAA	GACTCTACTT	CTGCTCCTGT	1200
CCGCATCGCC	GACTTTACTT	CAAAAATCGG	1260
CCAAGACATC	AAGGGTATGA	AAATCGCTTT	1320
GCCTAAGGAA	TACCTAGGCG	AAGGAATTGA	1380
TCCAGAGGTT	AAGGAAACAA	TCTTAAACGC	1440
GGCCAAACAC	TTTGAAAAAT	TGGGTGCTAT	1500
CGTCGAAGAA	GTCAGCCTTC	CTCACTCTAA	1560
ATACGGTGTT	GCCGTTTATT	ACATCATCGC	1620
TTCATCAGAA	GCTTCATCAA	ACTTGCAACG	1680
CTTCGACGGT	ATCCGTTACG	GCTATCGCGC	1740
AGAAGATGCA	ACCAACCTTG	ATGAAATCTA	1800
TGTAAACAGC	CGAAGCCAAG	GTTTTGGTGA	1860
AGAGGTAAAA	CGTCGTATCA	TGCTGGGTAC	1920
TTTCAGTCTT	TCATCAGGTT	ACTATGATGC	1980
CTACTACAAA	AAGGCTGGTC	AAGTCCGTAC	2040
CCTCATCATT	CAAGATTTTCG	AAAAAGTCTT	2100
CGCGGATTAC	GATTTGATTT	TGGGTCCAAC	2160
TGCTCCAAGT	GTTGCCTATG	ACTTGGATTG	2220
TCTCAACCAT	GACCCAGTTG	CCATGTACTT	2280
AGCCGACCTA	TTGACCATACTG	TAAACTTGGCAGGACTG	2340
CCTGGAATTT	CGATTCCTGC	TGGATTCTCT	2400
CAAGGTCTAC	CTGTCGGACT	CCAATTGATT	2460
GGTCCCAAGT	ACTCTGAGGA	AACCATTTAC	2520
CAAGCTGCTG	CTGCTTTTGA	AGCAACAACA	2580
GACTACCACA	AACAACAACC	CGTGATTTTT	2640
GGAGGTGACA	AC		2700

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 487 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr	Phe	Asn	Asn	Lys	Thr	Ile	Glu	Glu	Leu	His	Asn	Leu	Leu	Val	Ser	1	5	10	15
Lys	Glu	Ile	Ser	Ala	Thr	Glu	Leu	Thr	Gln	Ala	Thr	Leu	Glu	Asn	Ile	20	25	30	
Lys	Ser	Arg	Glu	Glu	Ala	Leu	Asn	Ser	Phe	Val	Thr	Ile	Ala	Glu	Glu	35	40	45	
Gln	Ala	Leu	Val	Gln	Ala	Lys	Ala	Ile	Asp	Glu	Ala	Gly	Ile	Asp	Ala	50	55	60	
Asp	Asn	Val	Leu	Ser	Gly	Ile	Pro	Leu	Ala	Val	Lys	Asp	Asn	Ile	Ser	65	70	75	80
Thr	Asp	Gly	Ile	Leu	Thr	Thr	Ala	Ala	Ser	Lys	Met	Leu	Tyr	Asn	Tyr	85	90	95	
Glu	Pro	Ile	Phe	Asp	Ala	Thr	Ala	Val	Ala	Asn	Ala	Lys	Thr	Lys	Gly	100	105	110	
Met	Ile	Val	Val	Gly	Lys	Thr	Asn	Met	Asp	Glu	Phe	Ala	Met	Gly	Gly	115	120	125	
Ser	Gly	Glu	Thr	Ser	His	Tyr	Gly	Ala	Thr	Lys	Asn	Ala	Trp	Asn	His	130	135	140	
Ser	Lys	Val	Pro	Gly	Gly	Ser	Ser	Ser	Gly	Ser	Ala	Ala	Ala	Val	Ala	145	150	155	160
Ser	Gly	Gln	Val	Arg	Leu	Ser	Leu	Gly	Ser	Asp	Thr	Gly	Gly	Ser	Ile	165	170	175	
Arg	Gln	Pro	Ala	Ala	Phe	Asn	Gly	Ile	Val	Gly	Leu	Lys	Pro	Thr	Tyr	180	185	190	
Gly	Thr	Val	Ser	Arg	Phe	Gly	Leu	Ile	Ala	Phe	Gly	Ser	Ser	Leu	Asp	195	200	205	
Gln	Ile	Gly	Pro	Phe	Ala	Pro	Thr	Val	Lys	Glu	Asn	Ala	Leu	Leu	Leu	210	215	220	
Asn	Ala	Ile	Ala	Ser	Glu	Asp	Ala	Lys	Asp	Ser	Thr	Ser	Ala	Pro	Val	225	230	235	240
Arg	Ile	Ala	Asp	Phe	Thr	Ser	Lys	Ile	Gly	Gln	Asp	Ile	Lys	Gly	Met	245	250	255	
Lys	Ile	Ala	Leu	Pro	Lys	Glu	Tyr	Leu	Gly	Glu	Gly	Ile	Asp	Pro	Glu	260	265	270	
Val	Lys	Glu	Thr	Ile	Leu	Asn	Ala	Ala	Lys	His	Phe	Glu	Lys	Leu	Gly	275	280	285	
Ala	Ile	Val	Glu	Glu	Val	Ser	Leu	Pro	His	Ser	Lys	Tyr	Gly	Val	Ala	290	295	300	

Val Tyr Tyr Ile Ile Ala Ser Ser Glu Ala Ser Ser Asn Leu Gln Arg  
 305 310 315 320  
 Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Ala Glu Asp Ala Thr Asn Leu  
 325 330 335  
 Asp Glu Ile Tyr Val Asn Ser Arg Ser Gln Gly Phe Gly Glu Glu Val  
 340 345 350  
 Lys Arg Arg Ile Met Leu Gly Thr Phe Ser Leu Ser Ser Gly Tyr Tyr  
 355 360 365  
 Asp Ala Tyr Tyr Lys Lys Ala Gly Gln Val Arg Thr Leu Ile Ile Gln  
 370 375 380  
 Asp Phe Glu Lys Val Phe Ala Asp Tyr Asp Leu Ile Leu Gly Pro Thr  
 385 390 395 400  
 Ala Pro Ser Val Ala Tyr Asp Leu Asp Ser Leu Asn His Asp Pro Val  
 405 410 415  
 Ala Met Tyr Leu Ala Asp Leu Leu Thr Ile Pro Val Asn Leu Ala Gly  
 420 425 430  
 Leu Pro Gly Ile Ser Ile Pro Ala Gly Phe Ser Gln Gly Leu Pro Val  
 435 440 445  
 Gly Leu Gln Leu Ile Gly Pro Lys Tyr Ser Glu Glu Thr Ile Tyr Gln  
 450 455 460  
 Ala Ala Ala Ala Phe Glu Ala Thr Thr Asp Tyr His Lys Gln Gln Pro  
 465 470 475 480  
 Val Ile Phe Gly Gly Asp Asn  
 485

## (2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 433 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CTTTACAGGT AAACAAC TAC AAGTCGGCGA CAAGGCGCTT GATTTTCTC TTACTACAAC	60
AGATCTTTCT AAAAAATCTC TGGCTGATTT TGATGGCAAG AAAAAAGTCT TGAGTGTCGT	120
TCCTTCTATC GATACAGGCA TCTGCTCAAC TCAAACACGT CGTTTTAATG AAGAATTGGC	180
TGGACTGGAC AACACGGTCG TATTGACTGT TTCAATGGAC CTACCTTTTG CTCAAAAACG	240
TTGGTGCGGT GCTGAAGGCC TTGACAATGC CATTATGCTT TCAGACTACT TTGACCATTC	300
TTTCGGGCGC GATTATGCC TCTTGATCAA CGAATGGCAC CTATTAGCAC GCGCAGTCTT	360
TGTCCTCGAT ACTGACAATA CGATTCGCTA CGTTGAATAC GTGGATAATA TCAATTCTGA	420
GCCAAACTTC GAA	433

## (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

Phe Thr Gly Lys Gln Leu Gln Val Gly Asp Lys Ala Leu Asp Phe Ser
1          5          10          15
Leu Thr Thr Thr Asp Leu Ser Lys Lys Ser Leu Ala Asp Phe Asp Gly
          20          25          30
Lys Lys Lys Val Leu Ser Val Val Pro Ser Ile Asp Thr Gly Ile Cys
          35          40          45
Ser Thr Gln Thr Arg Arg Phe Asn Glu Glu Leu Ala Gly Leu Asp Asn
          50          55          60
Thr Val Val Leu Thr Val Ser Met Asp Leu Pro Phe Ala Gln Lys Arg
65          70          75          80
Trp Cys Gly Ala Glu Gly Leu Asp Asn Ala Ile Met Leu Ser Asp Tyr
          85          90          95
Phe Asp His Ser Phe Gly Arg Asp Tyr Ala Leu Leu Ile Asn Glu Trp
          100          105          110
His Leu Leu Ala Arg Ala Val Phe Val Leu Asp Thr Asp Asn Thr Ile
          115          120          125
Arg Tyr Val Glu Tyr Val Asp Asn Ile Asn Ser Glu Pro Asn Phe Glu
          130          135          140

```

## (2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 724 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

CCAGGCTGAT ACAAGTATCG CAGACATTCA AAAAAGAGGC GAACTGGTTG TCGGTGTCAA      60
ACAAGACGTT CCCAATTTTG GTTACAAnGA TCCCAAGACC GGTACTTATT CTGGTATCGA      120
AaCCGACTTG GCCAAGATGG TAGCTGATGA ACTCAAGGTC AAGATTGCTT ATGTGCCGGT      180
TACAGCACAA ACCGCGGGCC CCCTTCTAGA CAATGAACAG GTCGATATGG ATATCGCGAC      240
CTTTACCATC ACGGACGAAC GCAAAAAAAct CTACAActTT ACCAGTCCCT ACTACACAGA      300
CGCTTCTGGA TTTTGTGTCA ATAAATCTGC CAAAATCAAA AAGATTGAGG ACCTAAACGG      360

```

```

CAAAACCATC GGAGTCGCCC AAGGTTCTAT CACCCAACGC CTGATTACTG AACTGGGTAA      420
AAAGAAAGGT CTGAAGTTTA AATTCGTCGA ACTTG GTTCC TACCCAGAAT TGATTACTTC      480
CCTGCACGCT CATCGTATCG ATACCTTTTC CGTTGACCGC TCTATTCTAT CTGGCTACAC      540
TAGTAAACGG ACAGCACTAC TAGATGATAG TTTCAAGCCA TCTGACTACG GTATTGTTAC      600
CAAGAAATCA AATACAGAGC TCAACGACTA TCTTGATAAC TTGGTTACTA AATGGAGCAA      660
GGATGGTAGT TTGCAGAAAC TTTATGACCG TTACAAGCTC AAACCATCTA GCCATACTGC      720
AGAT                                                                    724

```

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

Gln Ala Asp Thr Ser Ile Ala Asp Ile Gln Lys Arg Gly Glu Leu Val
1          5          10          15
Val Gly Val Lys Gln Asp Val Pro Asn Phe Gly Tyr Xaa Asp Pro Lys
20        25        30
Thr Gly Thr Tyr Ser Gly Ile Glu Thr Asp Leu Ala Lys Met Val Ala
35        40        45
Asp Glu Leu Lys Val Lys Ile Arg Tyr Val Pro Val Thr Ala Gln Thr
50        55        60
Arg Gly Pro Leu Leu Asp Asn Glu Gln Val Asp Met Asp Ile Ala Thr
65        70        75        80
Phe Thr Ile Thr Asp Glu Arg Lys Lys Leu Tyr Asn Phe Thr Ser Pro
85        90        95
Tyr Tyr Thr Asp Ala Ser Gly Phe Leu Val Asn Lys Ser Ala Lys Ile
100       105       110
Lys Lys Ile Glu Asp Leu Asn Gly Lys Thr Ile Gly Val Ala Gln Gly
115       120       125
Ser Ile Thr Gln Arg Leu Ile Thr Glu Leu Gly Lys Lys Lys Gly Leu
130       135       140
Lys Phe Lys Phe Val Glu Leu Gly Ser Tyr Pro Glu Leu Ile Thr Ser
145       150       155       160
Leu His Ala His Arg Ile Asp Thr Phe Ser Val Asp Arg Ser Ile Leu
165       170       175
Ser Gly Tyr Thr Ser Lys Arg Thr Ala Leu Leu Asp Asp Ser Phe Lys
180       185       190
Pro Ser Asp Tyr Gly Ile Val Thr Lys Lys Ser Asn Thr Glu Leu Asn

```

195	200	205
Asp Tyr Leu Asp Asn Leu Val Thr Lys Trp Ser Lys Asp Gly Ser Leu		
210	215	220
Gln Lys Leu Tyr Asp Arg Tyr Lys Leu Lys Pro Ser Ser His Thr Ala		
225	230	235 240
Asp		

## (2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1279 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTCTGTATCA TTTGAAAACA AAGAAACAAA CCGTGGTGTC TTgACTTTCA CTATCTCTCA	60
AGACCAAATC AAACCAGAAT TGGACCGTGT CTTCAAGtCA GTGAAGAAAT CTCTTAATGT	120
TCCAGGTTTC CGTAAAGGTC ACCTTCCACG CCCTATCTTC GACCAAAAAT TTGGTGAAGA	180
AGCTCTTTAT CAAGATGCAA TGAACGCACT TTTGCCAAAC GCTTATGAAG CAGCTGTAAA	240
AGAAGCTGGT CTTGAAGTGG TTGCCCAACC AAAAATTGAC GTAACttCAA TGGAAAAAGG	300
TCAAGACTGG GTTATCACTG CTGAAGTCGT TACAAAACCT GAAGTAAAAT TGGGTGACTA	360
CAAAAACCTT GAAGTATCAG TTGATGTAGA AAAAGAAGTA ACTGACGCTG ATGTCTGAAGA	420
CGGTATCGAA CGCGAACGCA ACAACCTGGC TGAATTGGTT ATCAAGGAAG CTGCTGCTGA	480
AAACGGCGAC ACTGTTGTGA TCGACTTCGT TGGTtCTATC GACGGTGTTG AATTTGACGG	540
TGGAAAAGGT GAAAACttCT CACTTGGACT TGGTTCAGGT CAATTCATCC CTGGTTTCGA	600
AGACCAATTG GTAGGTCACT CAGCTGGCGA AACCgTTGAT GTTATCGTAA CATTCCCAGA	660
AGACTACCAA GCAGAAGACC TTGCAGGTAA AGAAGCTAAA TTCGTGACAA CTATCCACGA	720
AGTAAAAGCT AAAGAAGTTC CGGCTCTTGA CGATGAACtt GCAAAAGACA TTGATGAAGA	780
AGTTGAAACA CTTGCTGACT TGAAAGAAAA ATACAGCAAA GAATTGGCTG CTGCTAAAGA	840
AGAAGCTTAC AAAGATGCAG TTGAAGGTGC AGCAATTGAT ACAGCTGTAG AAAATGCTGA	900
AATCGTAGAA CTTCCAGAAG AAATGATCCA TGAAGAAGTT CACCGTTCAG TAAATGAATT	960
CCTTGGAAT TTGCAACGTC AAGGGATCAA CCCTGACATG TACTTCCAAA TCACTGGAAC	1020
TACTCAAGAA GACCTTCACA ACCAATACCA AGCAGAAGCT GAGTCACGTA CTAAGACTAA	1080
CCTTGTTATC GAAGCAGTTG CCAAAGCTGA AGGATTTGAT GCTTCAGAAG AAGAAATCCA	1140
AAAAGAAGTT GAGCAATTGG CAGCAGACTA CAACATGGAA GTTGCACAAG TTCAAAACTT	1200
GCTTTCAGCT GACATGTTGA AACATGATAT CACTATCAAA AAAGCTGTTG AATTGATCAC	1260

AAGCACAGCA ACAGTAAAA

1279

## (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 426 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Val Ser Phe Glu Asn Lys Glu Thr Asn Arg Gly Val Leu Thr Phe  
 1 5 10 15  
 Thr Ile Ser Gln Asp Gln Ile Lys Pro Glu Leu Asp Arg Val Phe Lys  
 20 25 30  
 Ser Val Lys Lys Ser Leu Asn Val Pro Gly Phe Arg Lys Gly His Leu  
 35 40 45  
 Pro Arg Pro Ile Phe Asp Gln Lys Phe Gly Glu Glu Ala Leu Tyr Gln  
 50 55 60  
 Asp Ala Met Asn Ala Leu Leu Pro Asn Ala Tyr Glu Ala Ala Val Lys  
 65 70 75 80  
 Glu Ala Gly Leu Glu Val Val Ala Gln Pro Lys Ile Asp Val Thr Ser  
 85 90 95  
 Met Glu Lys Gly Gln Asp Trp Val Ile Thr Ala Glu Val Val Thr Lys  
 100 105 110  
 Pro Glu Val Lys Leu Gly Asp Tyr Lys Asn Leu Glu Val Ser Val Asp  
 115 120 125  
 Val Glu Lys Glu Val Thr Asp Ala Asp Val Glu Glu Arg Ile Glu Arg  
 130 135 140  
 Glu Arg Asn Asn Leu Ala Glu Leu Val Ile Lys Glu Ala Ala Ala Glu  
 145 150 155 160  
 Asn Gly Asp Thr Val Val Ile Asp Phe Val Gly Ser Ile Asp Gly Val  
 165 170 175  
 Glu Phe Asp Gly Gly Lys Gly Glu Asn Phe Ser Leu Gly Leu Gly Ser  
 180 185 190  
 Gly Gln Phe Ile Pro Gly Phe Glu Asp Gln Leu Val Gly His Ser Ala  
 195 200 205  
 Gly Glu Thr Val Asp Val Ile Val Thr Phe Pro Glu Asp Tyr Gln Ala  
 210 215 220  
 Glu Asp Leu Ala Gly Lys Glu Ala Lys Phe Val Thr Thr Ile His Glu  
 225 230 235 240  
 Val Lys Ala Lys Glu Val Pro Ala Leu Asp Asp Glu Leu Ala Lys Asp  
 245 250 255

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 490 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TGGTCAAAAG	GAAAGTCAGA	CAGGAAAGGG	GATGAAAATT	GTGACCAGTT	TTTATCCTAT	60
CTACGCTATG	GTTAAGGAAG	TATCTGGTGA	CTTGAATGAT	GTTCGGATGA	TTCAGTCAAG	120
TAGTGGTATT	CACTCCTTTG	AACCTTCGGC	AAATGATATC	GCAGCCATCT	ATGATGCAGA	180
TGTCTTTGTT	TACCATTCTC	ATACACTCGA	ATCTTGGGCA	GGAAGTCTGG	ATCCAAATCT	240
AAAAAAATCC	AAAGTGAAGG	TCTTAGAGGC	TTCTGAGGGA	ATGACCTTGG	AACGTGTCCC	300
TGGACTAGAG	GATGTGGAAG	CAGGGGATGG	AGTTGATGAA	AAAACGCTCT	ATGACCCTCA	360
CACATGGCTA	GATCCTGAAA	AAGCTGGAGA	AGAAGCCCCA	ATTATCGCTG	ATAAACTTTC	420
AGAGGTGGAT	AGTGAGCATA	AAGAGACTTA	TCAAAAAAAT	GCGCAACCTT	TATCAAAAAA	480
GCTCAGGAAT						490

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 163 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- ```

SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1006 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| GAAGGATAGA | TATATTTTAG | CATTTGAGAC | ATCCTGTGAT | GAGACCAAGTG | TCGCCGTCTT | 60  |
| GAAAAACGAC | GATGAGCTCT | TGTCCAATGT | CATTGCTAGT | CAAATTGAGA  | GTCACAAACG | 120 |
| TTTTGGTGGC | GTAGTGCCCG | AAGTAGCCAG | TCGTCACCAT | GTCGAGGTCA  | TTACAGCCTG | 180 |
| TATCGAGGAG | GCATTGGCAG | AAGCAGGGAT | TACCGAAGAG | GACGTGACAG  | CTGTTGCGGT | 240 |

```

TACCTACGGA CCAGGCTTGG TCGGAGCCTT GCTAGTTGGT TTGTCAGCTG CCAAGGCCTT      300
TGCTTGCGGCT CACGGACTTC CACTGATTCC TGTTAATCAC ATGGCTGGGC ACCTCATGGC      360
AGCTCAGAGT GTGGAGCCTT TGGAGTTTCC CTTGCTAGCC CTCTTGGTCA GCGGCGGACA      420
CACAGAGTTG GTTTATGTTT CGGAGGCAGG AGATTATAAG ATTGTTGGGG AAACCCGTGA      480
TGATGCGGTT GGTGAGGCTT ATGATAAGGT CGGCCGTGTC ATGGGCTTGA CCTATCCTGC      540
AGGTCGTGAG ATTGACGAGC TGGCTCATCA GGGGCAGGAT ATTTATGATT TCCCCCGTGC      600
CATGATTAAG GAAGATAATC TGGAGTTCTC CTTCTCAGGT TTGAAATCTG CCTTTATCAA      660
TCTTCATCAC AATGCCGAGC AAAAGGGAGA AAGCCTGTCT ACAGAAGATT TGTGTGCTTC      720
CTTCCAAGCA GCAGTTATGG ACATTCTCAT GGCAAAAACC AAGAAGGCTT TGGAGAAATA      780
TCCTGTAAAA ATCCTAGTTG TGGCAGGTGG TGTGGCAGCC AATAAAGGTC TCAGAGAACG      840
CCTAGCAGCC GAAATCACAG ATGTCAAGGT TATCATCCCC CCTCTGCGAC TCTGCGGAGA      900
CAATGCAGGT ATGATTGCCT ATGCCAGCGT CAGCNAGTGG AACAAAGAAA ACTTCGCAGG      960
CTGGGACCTC AATGCCAAAC CAAGTCTTGC CTTTGATACC ATGGAA                      1006

```

## (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

Lys Asp Arg Tyr Ile Leu Ala Phe Glu Thr Ser Cys Asp Glu Thr Ser
1           5           10           15
Val Ala Val Leu Lys Asn Asp Asp Glu Leu Leu Ser Asn Val Ile Ala
20          25          30
Ser Gln Ile Glu Ser His Lys Arg Phe Gly Gly Val Val Pro Glu Val
35          40          45
Ala Ser Arg His His Val Glu Val Ile Thr Ala Cys Ile Glu Glu Ala
50          55          60
Leu Ala Glu Ala Gly Ile Thr Glu Glu Asp Val Thr Ala Val Ala Val
65          70          75          80
Thr Tyr Gly Pro Gly Leu Val Gly Ala Leu Leu Val Gly Leu Ser Ala
85          90          95
Ala Lys Ala Phe Ala Trp Ala His Gly Leu Pro Leu Ile Pro Val Asn
100         105         110
His Met Ala Gly His Leu Met Ala Ala Gln Ser Val Glu Pro Leu Glu
115        120        125

```

Phe Pro Leu Leu Ala Leu Leu Val Ser Gly Gly His Thr Glu Leu Val  
 130 135 140  
 Tyr Val Ser Glu Ala Gly Asp Tyr Lys Ile Val Gly Glu Thr Arg Asp  
 145 150 155 160  
 Asp Ala Val Gly Glu Ala Tyr Asp Lys Val Gly Arg Val Met Gly Leu  
 165 170 175  
 Thr Tyr Pro Ala Gly Arg Glu Ile Asp Glu Leu Ala His Gln Gly Gln  
 180 185 190  
 Asp Ile Tyr Asp Phe Pro Arg Ala Met Ile Lys Glu Asp Asn Leu Glu  
 195 200 205  
 Phe Ser Phe Ser Gly Leu Lys Ser Ala Phe Ile Asn Leu His His Asn  
 210 215 220  
 Ala Glu Gln Lys Gly Glu Ser Leu Ser Thr Glu Asp Leu Cys Ala Ser  
 225 230 235 240  
 Phe Gln Ala Ala Val Met Asp Ile Leu Met Ala Lys Thr Lys Lys Ala  
 245 250 255  
 Leu Glu Lys Tyr Pro Val Lys Ile Leu Val Val Ala Gly Gly Val Ala  
 260 265 270  
 Ala Asn Lys Gly Leu Arg Glu Arg Leu Ala Ala Glu Ile Thr Asp Val  
 275 280 285  
 Lys Val Ile Ile Pro Pro Leu Arg Leu Cys Gly Asp Asn Ala Gly Met  
 290 295 300  
 Ile Ala Tyr Ala Ser Val Ser Xaa Trp Asn Lys Glu Asn Phe Ala Gly  
 305 310 315 320  
 Trp Asp Leu Asn Ala Lys Pro Ser Leu Ala Phe Asp Thr Met Glu  
 325 330 335

## (2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1000 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGTAGTTAAA GTTGGTATTA ACGGTTTCGG ACGTATCGGT CGTCTTGCTT TCCGTCGTAT | 60  |
| CCAAAACGTA GAAGGTGTTG AAGTTACACG CATCAACGAC CTTACAGATC CAGTTATGCT | 120 |
| TGCACACTTG TTGAAATACG ACACAACTCA AGGTCGTTTC GACGGTACTG TTGAAGTTAA | 180 |
| AGAAGGTGGA TTTGAAGTTA ACGGTAAATT CATCAAAGTT TCTGCTGAAC GTGATCCAGA | 240 |
| ACAAATCGAC TGGGCTACTG ACGGTGTAGA AATCGTTCTT GAAGCTACTG GTTCTTTGCT | 300 |
| TAAGAAAGAA GCAGCTGAAA AACACCTTAA AGGTGGAGCT AAAAAAGTTG TTATCACTGC | 360 |
| TCCTGGTGGA AACGACGTTA AAACAGTTGT ATTCAACACT AACCACGACG TTCTTGACGG | 420 |

```

TACTGAAACA GTTATCTCAG GTGCTTCATG TACTACAAAC TGCTTGGCTC CAATGGCTAA      480
AGCTCTTCAA GACAACTTTG GTGTTGTTGA AGGATTGATG ACTACTATCC ACGCTTACAC      540
TGGTGACCAA ATGATCCTTG ACGGACCACA CCGTGGTGGT GACCTTCGCC GTGCTCGCGC      600
TGGTGCTGCA AACATCGTTC CTAAC TCAAC TGGTGCTGCA AAAGCTATCG GTCTTGTAAT      660
CCCAGAATTG AATGGTAAAC TTGACGGATC TGCACAACGC GTTCCAAC TC CAACTGGATC      720
AGTTACTGAA TTGGTAGCAG TTCTTGAAAA GAACGTTACT GTTGATGAAG TGAACGCAGC      780
TATGAAAGCA GCTTCAAACG AATCATACGG TTACACAGAA GATCCAATCG TATCTTCAGA      840
TATCGTAGGT ATGTCTTACG GTTCATTGTT TGACGCAACT CAAACTAAAG TTCTTGACGT      900
TGACGGTAAA CAATTGGTTA AAGTTGTATC ATGGTACGAC AACGAAATGT CATACTGTC      960
ACAACTTGTT CGTACTCTTG GAATACTTCG CAAAATTGTC      1000

```

## (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 333 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```

Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Ala
1          5          10          15
Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile Asn
20        25        30
Asp Leu Thr Asp Pro Val Met Leu Ala His Leu Leu Lys Tyr Asp Thr
35        40        45
Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly Phe
50        55        60
Glu Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Arg Asp Pro Glu
65        70        75        80
Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala Thr
85        90        95
Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu Lys Gly Gly
100       105       110
Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val Lys Thr
115       120       125
Val Val Phe Asn Thr Asn His Asp Val Leu Asp Gly Thr Glu Thr Val
130       135       140
Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys
145       150       155       160

```

Ala Leu Gln Asp Asn Phe Gly Val Val Glu Gly Leu Met Thr Thr Ile  
165 170 175  
His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His Arg Gly  
180 185 190  
Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val Pro Asn  
195 200 205  
Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu Leu Asn  
210 215 220  
Gly Lys Leu Asp Gly Ser Ala Gln Arg Val Pro Thr Pro Thr Gly Ser  
225 230 235 240  
Val Thr Glu Leu Val Ala Val Leu Glu Lys Asn Val Thr Val Asp Glu  
245 250 255  
Val Asn Ala Ala Met Lys Ala Ala Ser Asn Glu Ser Tyr Gly Tyr Thr  
260 265 270  
Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Tyr Gly Ser  
275 280 285  
Leu Phe Asp Ala Thr Gln Thr Lys Val Leu Asp Val Asp Gly Lys Gln  
290 295 300  
Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr Thr Ala  
305 310 315 320  
Gln Leu Val Arg Thr Leu Gly Ile Leu Arg Lys Asn Cys  
325 330

## (2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2389 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTCTTACGAG TTGGGACTGT ATCAAGCTAG AACGGTTAAG GAAAATAATC GTGTTTCCTA  | 60  |
| TATAGATGGA AAACAAGCGA CGCAAAAAAC GGAGAATTTG ACTCCTGATG AGGTTAGCAA  | 120 |
| GCGTGAAGGA ATCAATGCTG AGCAAATCGT CATCAAGATA ACAGACCAAG GCTATGTCAC  | 180 |
| TTCACATGGC GACCACTATC ATTATTACAA TGGTAAGGTT CCTTATGACG CTATCATCAG  | 240 |
| TGAAGAATTA CTCATGAAAG ATCCAAACTA TAAGCTAAAA GATGAGGATA TTGTTAATGA  | 300 |
| GGTCAAGGGT GGATATGTTA TCAAGGTAGA TGGAAAATAC TATGTTTACC TTAAGGATGC  | 360 |
| TGCCCACGCG GATAACGTCC GTACAAAAGA GGAAATCAAT CGACAAAAAC AAGAGCATAG  | 420 |
| TCAACATCGT GAAGGTGGAA CTCCAAGAAA CGATGGTGCT GTTGCCTTGG CACGTTTCGCA | 480 |
| AGGACGCTAT ACTACAGATG ATGGTTATAT CTTTAATGCT TCTGATATCA TAGAGGATAC  | 540 |
| TGGTGATGCT TATATCGTTC CTCATGGAGA TCATTACCAT TACATTCCTA AGAATGAGTT  | 600 |
| ATCAGCTAGC GAGTTGGCTG CTGCAGAAGC CTTCTATCT GGTGAGGAA ATCTGTCAAA    | 660 |

|             |             |            |            |            |            |      |
|-------------|-------------|------------|------------|------------|------------|------|
| TTCAAGAACC  | TATCGCCGAC  | AAAATAGCGA | TAACACTTCA | AGAACAAACT | GGGTACCTTC | 720  |
| TGTAAGCAAT  | CCAGGAAC TA | CAAATACTAA | CACAAGCAAC | AACAGCAACA | CTAACAGTCA | 780  |
| AGCAAGTCAA  | AGTAATGACA  | TTGATAGTCT | CTTGAAACAG | CTCTACAAAC | TGCCTTTGAG | 840  |
| TCAACGACAT  | GTAGAATCTG  | ATGGCCTTGT | CTTTGATCCA | GCACAAATCA | CAAGTCGAAC | 900  |
| AGCTAGAGGT  | GTTGCAGTGC  | CACACGGAGA | TCATTACCAC | TTCATCCCTT | ACTCTCAAAT | 960  |
| GTCTGAATTG  | GAAGAACGAA  | TCGCTCGTAT | TATTCCCCTT | CGTTATCGTT | CAAACCATTG | 1020 |
| GGTACCAGAT  | TCAAGGCCAG  | AACAACCAAG | TCCACAACCG | ACTCCGGAAC | CTAGTCCAGG | 1080 |
| CCCGCAACCT  | GCACCAAATC  | TTAAAATAGA | CTCAAATTCT | TCTTTGGTTA | GTCAGCTGGT | 1140 |
| ACGAAAAGTT  | GGGGAAGGAT  | ATGTATTCTG | AGAAAAGGGC | ATCTCTCGTT | ATGTCTTTGC | 1200 |
| GAAAGATTTA  | CCATCTGAAA  | CTGTTAAAAA | TCTTGAAAGC | AAGTTATCAA | AACAAGAGAG | 1260 |
| TGTTTCACAC  | ACTTTAACTG  | CTAAAAAAGA | AAATGTTGCT | CCTCGTGACC | AAGAATTTTA | 1320 |
| TGATAAAGCA  | TATAATCTGT  | TAAGTGAGGC | TCATAAAGCC | TTGTTTGNA  | ATAAGGGTCG | 1380 |
| TAATTCTGAT  | TTCCAAGCCT  | TAGACAAATT | ATTAGAACGC | TTGAATGATG | AATCGACTAA | 1440 |
| TAAAGAAAAA  | TTGGTAGATG  | ATTTATTGGC | ATTCCTAGCA | CCAATTACCC | ATCCAGAGCG | 1500 |
| ACTTGCCAAA  | CCAAATTCTC  | AAATTGAGTA | TACTGAAGAC | GAAGTTCGTA | TTGCTCAATT | 1560 |
| AGCTGATAAG  | TATACAACGT  | CAGATGGTTA | CATTTTGTG  | GAACATGATA | TAATCAGTGA | 1620 |
| TGAAGGAGAT  | GCATATGTAA  | CGCCTCATAT | GGGCCATAGT | CACTGGATTG | GAAAAGATAG | 1680 |
| CCTTTCTGAT  | AAGGAAAAAG  | TTGCAGCTCA | AGCCTATACT | AAAGAAAAAG | GTATCTTACC | 1740 |
| TCCATCTCCA  | GACGCAGATG  | TTAAAGCAAA | TCCAAGTGG  | GATAGTGCAG | CAGCTATTTA | 1800 |
| CAATCGTG TG | AAAGGGGAAA  | AACGAATTCC | ACTCGTTCGA | CTTCCATATA | TGGTTGAGCA | 1860 |
| TACAGTTGAG  | GTTAAAAACG  | GTAATTTGAT | TATTCCTCAT | AAGGATCATT | ACCATAATAT | 1920 |
| TAAATTTGCT  | TGGTTTGATG  | ATCACACATA | CAAAGCTCCA | AATGGCTATA | CCTTGGAAGA | 1980 |
| TTTGT TTGCG | ACGATTAAGT  | ACTACGTAGA | ACACCCTGAC | GAACGTCCAC | ATTCTAATGA | 2040 |
| TGGATGGGGC  | AATGCCAGTG  | AGCATGTGTT | AGGCAAGAAA | GACCACAGTG | AAGATCCAAA | 2100 |
| TAAGAACTTC  | AAAGCGGATG  | AAGAGCCAGT | AGAGGAAACA | CCTGCTGAGC | CAGAAGTCCC | 2160 |
| TCAAGTAGAG  | ACTGAAAAAG  | TAGAAGCCCA | ACTCAAAGAA | GCAGAAGTTT | TGCTTGCGAA | 2220 |
| AGTAACGGAT  | TCTAGTCTGA  | AAGCCAATGC | AACAGAAACT | CTAGCTGGTT | TACGAAATAA | 2280 |
| TTTGACTCTT  | CAAATTATGG  | ATAACAATAG | TATCATGGCA | GAAGCAGAAA | AATTACTTGC | 2340 |
| GTTGT TAAAA | GGAAGTAATC  | CTTCATCTGT | AAGTAAGGAA | AAAAATAAAC |            | 2389 |

## (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 796 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Tyr | Glu | Leu | Gly | Leu | Tyr | Gln | Ala | Arg | Thr | Val | Lys | Glu | Asn | Asn | 1   | 5   | 10  | 15  |
| Arg | Val | Ser | Tyr | Ile | Asp | Gly | Lys | Gln | Ala | Thr | Gln | Lys | Thr | Glu | Asn | 20  | 25  | 30  |     |
| Leu | Thr | Pro | Asp | Glu | Val | Ser | Lys | Arg | Glu | Gly | Ile | Asn | Ala | Glu | Gln | 35  | 40  | 45  |     |
| Ile | Val | Ile | Lys | Ile | Thr | Asp | Gln | Gly | Tyr | Val | Thr | Ser | His | Gly | Asp | 50  | 55  | 60  |     |
| His | Tyr | His | Tyr | Tyr | Asn | Gly | Lys | Val | Pro | Tyr | Asp | Ala | Ile | Ile | Ser | 65  | 70  | 75  | 80  |
| Glu | Glu | Leu | Leu | Met | Lys | Asp | Pro | Asn | Tyr | Lys | Leu | Lys | Asp | Glu | Asp | 85  | 90  | 95  |     |
| Ile | Val | Asn | Glu | Val | Lys | Gly | Gly | Tyr | Val | Ile | Lys | Val | Asp | Gly | Lys | 100 | 105 | 110 |     |
| Tyr | Tyr | Val | Tyr | Leu | Lys | Asp | Ala | Ala | His | Ala | Asp | Asn | Val | Arg | Thr | 115 | 120 | 125 |     |
| Lys | Glu | Glu | Ile | Asn | Arg | Gln | Lys | Gln | Glu | His | Ser | Gln | His | Arg | Glu | 130 | 135 | 140 |     |
| Gly | Gly | Thr | Pro | Arg | Asn | Asp | Gly | Ala | Val | Ala | Leu | Ala | Arg | Ser | Gln | 145 | 150 | 155 | 160 |
| Gly | Arg | Tyr | Thr | Thr | Asp | Asp | Gly | Tyr | Ile | Phe | Asn | Ala | Ser | Asp | Ile | 165 | 170 | 175 |     |
| Ile | Glu | Asp | Thr | Gly | Asp | Ala | Tyr | Ile | Val | Pro | His | Gly | Asp | His | Tyr | 180 | 185 | 190 |     |
| His | Tyr | Ile | Pro | Lys | Asn | Glu | Leu | Ser | Ala | Ser | Glu | Leu | Ala | Ala | Ala | 195 | 200 | 205 |     |
| Glu | Ala | Phe | Leu | Ser | Gly | Arg | Gly | Asn | Leu | Ser | Asn | Ser | Arg | Thr | Tyr | 210 | 215 | 220 |     |
| Arg | Arg | Gln | Asn | Ser | Asp | Asn | Thr | Ser | Arg | Thr | Asn | Trp | Val | Pro | Ser | 225 | 230 | 235 | 240 |
| Val | Ser | Asn | Pro | Gly | Thr | Thr | Asn | Thr | Asn | Thr | Ser | Asn | Asn | Ser | Asn | 245 | 250 | 255 |     |
| Thr | Asn | Ser | Gln | Ala | Ser | Gln | Ser | Asn | Asp | Ile | Asp | Ser | Leu | Leu | Lys | 260 | 265 | 270 |     |
| Gln | Leu | Tyr | Lys | Leu | Pro | Leu | Ser | Gln | Arg | His | Val | Glu | Ser | Asp | Gly | 275 | 280 | 285 |     |
| Leu | Val | Phe | Asp | Pro | Ala | Gln | Ile | Thr | Ser | Arg | Thr | Ala | Arg | Gly | Val | 290 | 295 | 300 |     |

Ala Val Pro His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Gln Met  
 305 310 315 320  
 Ser Glu Leu Glu Glu Arg Ile Ala Arg Ile Ile Pro Leu Arg Tyr Arg  
 325 330 335  
 Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln Pro Ser Pro Gln  
 340 345 350  
 Pro Thr Pro Glu Pro Ser Pro Gly Pro Gln Pro Ala Pro Asn Leu Lys  
 355 360 365  
 Ile Asp Ser Asn Ser Ser Leu Val Ser Gln Leu Val Arg Lys Val Gly  
 370 375 380  
 Glu Gly Tyr Val Phe Glu Glu Lys Gly Ile Ser Arg Tyr Val Phe Ala  
 385 390 395 400  
 Lys Asp Leu Pro Ser Glu Thr Val Lys Asn Leu Glu Ser Lys Leu Ser  
 405 410 415  
 Lys Gln Glu Ser Val Ser His Thr Leu Thr Ala Lys Lys Glu Asn Val  
 420 425 430  
 Ala Pro Arg Asp Gln Glu Phe Tyr Asp Lys Ala Tyr Asn Leu Leu Thr  
 435 440 445  
 Glu Ala His Lys Ala Leu Phe Xaa Asn Lys Gly Arg Asn Ser Asp Phe  
 450 455 460  
 Gln Ala Leu Asp Lys Leu Leu Glu Arg Leu Asn Asp Glu Ser Thr Asn  
 465 470 475 480  
 Lys Glu Lys Leu Val Asp Asp Leu Leu Ala Phe Leu Ala Pro Ile Thr  
 485 490 495  
 His Pro Glu Arg Leu Gly Lys Pro Asn Ser Gln Ile Glu Tyr Thr Glu  
 500 505 510  
 Asp Glu Val Arg Ile Ala Gln Leu Ala Asp Lys Tyr Thr Thr Ser Asp  
 515 520 525  
 Gly Tyr Ile Phe Asp Glu His Asp Ile Ile Ser Asp Glu Gly Asp Ala  
 530 535 540  
 Tyr Val Thr Pro His Met Gly His Ser His Trp Ile Gly Lys Asp Ser  
 545 550 555 560  
 Leu Ser Asp Lys Glu Lys Val Ala Ala Gln Ala Tyr Thr Lys Glu Lys  
 565 570 575  
 Gly Ile Leu Pro Pro Ser Pro Asp Ala Asp Val Lys Ala Asn Pro Thr  
 580 585 590  
 Gly Asp Ser Ala Ala Ala Ile Tyr Asn Arg Val Lys Gly Glu Lys Arg  
 595 600 605  
 Ile Pro Leu Val Arg Leu Pro Tyr Met Val Glu His Thr Val Glu Val  
 610 615 620  
 Lys Asn Gly Asn Leu Ile Ile Pro His Lys Asp His Tyr His Asn Ile  
 625 630 635 640

Lys Phe Ala Trp Phe Asp Asp His Thr Tyr Lys Ala Pro Asn Gly Tyr  
                                 645                                650                                655  
 Thr Leu Glu Asp Leu Phe Ala Thr Ile Lys Tyr Tyr Val Glu His Pro  
                                 660                                665                                670  
 Asp Glu Arg Pro His Ser Asn Asp Gly Trp Gly Asn Ala Ser Glu His  
                                 675                                680                                685  
 Val Leu Gly Lys Lys Asp His Ser Glu Asp Pro Asn Lys Asn Phe Lys  
                                 690                                695                                700  
 Ala Asp Glu Glu Pro Val Glu Glu Thr Pro Ala Glu Pro Glu Val Pro  
                                 705                                710                                715                                720  
 Gln Val Glu Thr Glu Lys Val Glu Ala Gln Leu Lys Glu Ala Glu Val  
                                 725                                730                                735  
 Leu Leu Ala Lys Val Thr Asp Ser Ser Leu Lys Ala Asn Ala Thr Glu  
                                 740                                745                                750  
 Thr Leu Ala Gly Leu Arg Asn Asn Leu Thr Leu Gln Ile Met Asp Asn  
                                 755                                760                                765  
 Asn Ser Ile Met Ala Glu Ala Glu Lys Leu Leu Ala Leu Leu Lys Gly  
                                 770                                775                                780  
 Ser Asn Pro Ser Ser Val Ser Lys Glu Lys Ile Asn  
                                 785                                790                                795

## (2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1180 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| TACTGAGATG CATCATAATC TAGGAGCTGA AAAGCGTTCA GCAGTGGCTA CTACTATCGA   | 60  |
| TAGTTTTTAAG GAGCGAAGTC AAAAAGTCAG AGCACTATCT GATCCAAATG TGC GTTTTGT | 120 |
| TCCCTTCTTT GGCTCTAGTG AATGGCTTCG TTTTGACGGT GCTCATTCTG CGGTATTAGC   | 180 |
| TGAGAAATAC AATCGTTCCT ACCGTCCTTA TCTTTTAGGA CAGGGGGGAG CTGCATCGCT   | 240 |
| TAACCAATAT TTTGGAATGC AACAGATGTT ACCACAGCTG GAGAATAAAC AAGTTGTGTA   | 300 |
| TGTTATCTCA CCTCAGTGGT TCAGTAAAAA TGGCTATGAT CCAGCAGCCT TCCAGCAGTA   | 360 |
| TTTTAATGGA GACCAGTTGA CTAGTTTCT GAAACATCAA TCTGGGGATC AGGCTAGTCA    | 420 |
| ATATGCAGCG ACTCGCTTAC TGCAACAGTT CCCAAACGTA GCTATGAAGG ACCTGGTTCA   | 480 |
| GAAGTTGGCA AGTAAAGAAG AATTGTCGAC AGCAGACAAT GAAATGATTG AATTATTGGC   | 540 |
| TCGTTTTAAT GAACGCCAAG CTTCCCTTTT TGGTCAGTTT TCGGTTAGAG GCTATGTTAA   | 600 |
| CTACGATAAG CATGTAGCTA AGTATTTAAA AATCTTGCCA GACCAGTTTT CTTATCAGGC   | 660 |

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AATAGAAGAT GTTGTCAAAG CAGATGCTGA AAAAAATACT TCCAATAATG AGATGGGAAT      720
GGAAAATTAT TTCTATAATG AGCAGATCAA GAAGGATTTG AAGAAATTAA AGGATTCTCA      780
GAAAAGCTTT ACCTATCTCA AGTCGCCAGA GTATAATGNN TTGCAGTTGG TTTTAACACA      840
GTTTTCTAAA TCTAAGGTAA ACCCGATTTT TATCATTCCA CCTGTTAATA AAAAAATGGAT      900
GNACTATGCT GGTCTACGAG AGGATATGTA CCAACAAACG GTGCAGAAGA TTCGCTACCA      960
GTTAGAAAGT CAAGGTTTTA CCAATATAGC AGATTTTTTCT AAGGACGGCG GGGAGCCTTT 1020
CTTTATGAAG GACACCATTC ACCTTGTTTG GTTGGGTTTG TTGGCTTTTG ACAAGGCAGT 1080
TGATCCTTTC CTATCCAATC CCACACCAGC TCCGACTTAC CATCTGAATG AGCGCTTTTT 1140
CAGCAAAGAT TGGGCGACTT ATGATGGAGA TGTCAAAGAA      1180

```

## (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 393 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

Thr Glu Met His His Asn Leu Gly Ala Glu Lys Arg Ser Ala Val Ala
1          5          10          15
Thr Thr Ile Asp Ser Phe Lys Glu Arg Ser Gln Lys Val Arg Ala Leu
20        25        30
Ser Asp Pro Asn Val Arg Phe Val Pro Phe Phe Gly Ser Ser Glu Trp
35        40        45
Leu Arg Phe Asp Gly Ala His Ser Ala Val Leu Ala Glu Lys Tyr Asn
50        55        60
Arg Ser Tyr Arg Pro Tyr Leu Leu Gly Gln Gly Gly Ala Ala Ser Leu
65        70        75        80
Asn Gln Tyr Phe Gly Met Gln Gln Met Leu Pro Gln Leu Glu Asn Lys
85        90        95
Gln Val Val Tyr Val Ile Ser Pro Gln Trp Phe Ser Lys Asn Gly Tyr
100       105       110
Asp Pro Ala Ala Phe Gln Gln Tyr Phe Asn Gly Asp Gln Leu Thr Ser
115       120       125
Phe Leu Lys His Gln Ser Gly Asp Gln Ala Ser Gln Tyr Ala Ala Thr
130       135       140
Arg Leu Leu Gln Gln Phe Pro Asn Val Ala Met Lys Asp Leu Val Gln
145       150       155       160
Lys Leu Ala Ser Lys Glu Glu Leu Ser Thr Ala Asp Asn Glu Met Ile
165       170       175

```

Glu Leu Leu Ala Arg Phe Asn Glu Arg Gln Ala Ser Phe Phe Gly Gln  
 180 185 190  
 Phe Ser Val Arg Gly Tyr Val Asn Tyr Asp Lys His Val Ala Lys Tyr  
 195 200 205  
 Leu Lys Ile Leu Pro Asp Gln Phe Ser Tyr Gln Ala Ile Glu Asp Val  
 210 215 220  
 Val Lys Ala Asp Ala Glu Lys Asn Thr Ser Asn Asn Glu Met Gly Met  
 225 230 235 240  
 Glu Asn Tyr Phe Tyr Asn Glu Gln Ile Lys Lys Asp Leu Lys Lys Leu  
 245 250 255  
 Lys Asp Ser Gln Lys Ser Phe Thr Tyr Leu Lys Ser Pro Glu Tyr Asn  
 260 265 270  
 Xaa Leu Gln Leu Val Leu Thr Gln Phe Ser Lys Ser Lys Val Asn Pro  
 275 280 285  
 Ile Phe Ile Ile Pro Pro Val Asn Lys Lys Trp Met Xaa Tyr Ala Gly  
 290 295 300  
 Leu Arg Glu Asp Met Tyr Gln Gln Thr Val Gln Lys Ile Arg Tyr Gln  
 305 310 315 320  
 Leu Glu Ser Gln Gly Phe Thr Asn Ile Ala Asp Phe Ser Lys Asp Gly  
 325 330 335  
 Gly Glu Pro Phe Phe Met Lys Asp Thr Ile His Leu Gly Trp Leu Gly  
 340 345 350  
 Trp Leu Ala Phe Asp Lys Ala Val Asp Pro Phe Leu Ser Asn Pro Thr  
 355 360 365  
 Pro Ala Pro Thr Tyr His Leu Asn Glu Arg Phe Phe Ser Lys Asp Trp  
 370 375 380  
 Ala Thr Tyr Asp Gly Asp Val Lys Glu  
 385 390

## (2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1423 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGTTTTGAGA AAGTATTTGC AGGGGGCCCT GATTGAGTCG ATTGAGCAAG TGGAAAATGA | 60  |
| CCGTATTGTG GAAATTACAG TTTCCAATAA AAACGAGATT GGAGACCATA TCCAGGCTAC | 120 |
| CTTGATTATC GAAATTATGG GGAAACACAG TAATATTCTA CTGGTCGATA AAAGCAGTCA | 180 |
| TAAAATCCTC GAAGTTATCA AACACGTCGG CTTTTCACAA AATAGCTACC GCACCTTACT | 240 |
| TCCAGGATCG ACCTATATCG CTCCGCCAAG TACAAAATCT CTCAATCCTT TTAATATCAA | 300 |

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GGATGAAAAG CTCTTTGAAA TCCTGCAAAC CCAAGAACTA ACAGCAAAAA ATCTTCAAAG      360
CCTCTTTTCAA GGTCTGGGAC GCGATACGGC AAATGAATTG GAAAGGATAC TGGTTAGTGA      420
AAAACTTTCC GCTTTCGGAA ATTTTTTTCAA TCAAGAAACC AAGCCATGCT TGA CTGAGAC      480
TTCCTTCAGT CCAGTTCCTT TTGCAAATCA GGTGGGAGAG CCTTTTGCAA ATCTTTCTGA      540
TTTGTGGAC ACCTACTATA AGGATAAGGC TGAGCGCGAC CGCGTCAAAC AGCAGGCCAG      600
TGAAGTGAAT CGTCGTGTTG AAAATGAACT TCAGAAAAAC CGACACAAAC TCAAAAAACA      660
GGAAAAAGAG TTACTGGCGA CAGACAACGC TGAAGAATTT CGTCAAAAAG GAGAATTGCT      720
GACAACCTTC CTCCACCAAG TGCCTAACGA CCAAGACCAG GTTATCCTAG ACAACTACTA      780
TACCAACCAA CCTATCATGA TTGCGCTTGA TAAGGCTCTG ACTCCCAACC AGAATGCCCA      840
ACGCTATTTT AAACGGTATC AGAAACTCAA AGAAGCTGTC AAATACTTGA CTGATTTGAT      900
TGAAGAAACC AAAGCCACTA TTCTCTATCT GGAAAGTGTA GAAACCGTCC TCAACCAAGC      960
TGGACTGGAA GAAATCGCTG AAATCCGTGA AGAATTGATT CAAACAGGTT TTATCCGCAG     1020
AAGACAACGG GAGAAAATCC AGAAACGCAA AAAACTAGAA CAATATCTAG CAAGCGATGG     1080
CAAAACCATC ATCTATGTCG GACGAAACAA TCTTCAAAAT GAGGAATTGA CCTTTAAAAT     1140
GGCCCGCAAG GAGGAACTTT GGTTCATGC TAAGGACATT CCTGGAAGCC ATGTTGTCAT     1200
CTCAGGAAAT CTTGACCCAT CTGATGCAGT CAAGACAGAC GCAGCAGAGT TAGCTGCCTA     1260
CTTCTCTCAA GGGCGCCTGT CGAATCTGGT GCAGGTAGAT ATGATTGAAG TCAAAAAACT     1320
CAATAAACCA ACTGGTGGAA AACCCGGCTT TGTCACCTAC ACAGGACAAA AGACCCTCCG     1380
CGTCACACCA GACTCCAAAA AAATTGCATC CATGAAAAAA TCC                        1423

```

## (2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 474 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```

Val Leu Arg Lys Tyr Leu Gln Gly Ala Leu Ile Glu Ser Ile Glu Gln
1           5           10           15
Val Glu Asn Asp Arg Ile Val Glu Ile Thr Val Ser Asn Lys Asn Glu
20          25          30
Ile Gly Asp His Ile Gln Ala Thr Leu Ile Ile Glu Ile Met Gly Lys
35          40          45
His Ser Asn Ile Leu Leu Val Asp Lys Ser Ser His Lys Ile Leu Glu
50          55          60
Val Ile Lys His Val Gly Phe Ser Gln Asn Ser Tyr Arg Thr Leu Leu

```



Leu Ala Ala Tyr Phe Ser Gln Gly Arg Leu Ser Asn Leu Val Gln Val  
 420 425 430

Asp Met Ile Glu Val Lys Lys Leu Asn Lys Pro Thr Gly Gly Lys Pro  
 435 440 445

Gly Phe Val Thr Tyr Thr Gly Gln Lys Thr Leu Arg Val Thr Pro Asp  
 450 455 460

Ser Lys Lys Ile Ala Ser Met Lys Lys Ser  
 465 470

## (2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 544 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GACAACATTT ACTATCCATA CAGTAGAGTC AGCACCAGCA GAAGTGAAAG AAATTCTTGA | 60  |
| AACAGTAGAA AAAGACAACA ATGGCTATAT TCCCAACCTA ATCGGTCTCT TGGCCAATGC | 120 |
| CCCGACTGTT TTAGAAGCCT ACCAAATTGT CTCATCTATC CACCGTCGCA ACAGCCTGAC | 180 |
| ACCCGTTGAG CGTGAAGTGG TGCAAATCAC GGCAGCCGTG ACCAATGGTT GTGCCTTCTG | 240 |
| TGTCGCAGGT CACACAGCCT TTTCCATCAA ACAAATCCAG ATGAATGATG ACTTGATTCA | 300 |
| AGCTCTTCGC AATCGTACTC CAATTGAAAC AGATCCTAAA TTGGATACCC TAGCTAAGTT | 360 |
| TACCTTGGCA GTTATCAATA CCAAGGGTCG TGTAGGAGAT GAAGCCTTGT CTGAGTTTTT | 420 |
| AGAAGCTGGC TACACTCAAC AAAATGCCTT GGATGTGGTT TTTGGTGTCA GCCTAGCAAT | 480 |
| CCTCTGTAAC TATGCCAACA ACTTAGCTAA TACACCAATT AATCCAGAAT TGCAACCTTA | 540 |
| TGCC                                                              | 544 |

## (2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 181 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Thr Thr Phe Thr Ile His Thr Val Glu Ser Ala Pro Ala Glu Val Lys |  |
| 1 5 10 15                                                       |  |
| Glu Ile Leu Glu Thr Val Glu Lys Asp Asn Asn Gly Tyr Ile Pro Asn |  |
| 20 25 30                                                        |  |

Leu Ile Gly Leu Leu Ala Asn Ala Pro Thr Val Leu Glu Ala Tyr Gln  
           35                          40                          45  
 Ile Val Ser Ser Ile His Arg Arg Asn Ser Leu Thr Pro Val Glu Arg  
           50                          55                          60  
 Glu Val Val Gln Ile Thr Ala Ala Val Thr Asn Gly Cys Ala Phe Cys  
           65                          70                          75                          80  
 Val Ala Gly His Thr Ala Phe Ser Ile Lys Gln Ile Gln Met Asn Asp  
                           85                          90                          95  
 Asp Leu Ile Gln Ala Leu Arg Asn Arg Thr Pro Ile Glu Thr Asp Pro  
                           100                          105                          110  
 Lys Leu Asp Thr Leu Ala Lys Phe Thr Leu Ala Val Ile Asn Thr Lys  
           115                          120                          125  
 Gly Arg Val Gly Asp Glu Ala Leu Ser Glu Phe Leu Glu Ala Gly Tyr  
           130                          135                          140  
 Thr Gln Gln Asn Ala Leu Asp Val Val Phe Gly Val Ser Leu Ala Ile  
           145                          150                          155                          160  
 Leu Cys Asn Tyr Ala Asn Asn Leu Ala Asn Thr Pro Ile Asn Pro Glu  
                           165                          170                          175  
 Leu Gln Pro Tyr Ala  
                           180

## (2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 811 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGCTAAGGAA AGAGTGGATG TACTAGCTTA TAAACAGGGG TTGTTTGAAA CGAGAGAGCA | 60  |
| GGCCAAGCGA GGTGTGATGG CTGGCCTAGT CGTAGCAGTC CTTAATGGAG AACGGTTTGA | 120 |
| CAAGCCAGGA GAGAAAATTC CAGATGACAC CGAATTAAAA CTCAAGGGGG AGAAACTCAA | 180 |
| GTATGTCAGC CGTGGTGGTT TGAAACTGGA AAAGGCCTTG CAGGTCTTTG ATTTGTCGGT | 240 |
| GGATGGCGCG ACTACGATTG ATATCGGGGC CTCTACTGGA GGTTTTACCG ATGTCATGCT | 300 |
| ACAGAATAGT GCCAAGTTGG TCTTTGCAGT CGATGTTGGT ACCAATCAGT TGGCTTGGA  | 360 |
| ATTACGCCAA GACCCACGAG TTGTCAGCAT GGAGCAGTTC AATTTCCGCT ATGCTGAAAA | 420 |
| GACTGATTTT GAGCAGGAGC CGAGCTTTGC CAGTATTGAT GTGAGTTTCA TTTCCCTTAG | 480 |
| TCTGATTTTG CCAGCCTTGC ACCGTGTCTT GGCTGATCAA GGTCAGGTGG TAGCACTTGT | 540 |
| CAAACCTCAG TTTGAGGCAG GACGTGAGCA GATTGGGAAA AATGGAATTA TTCGAGATGC | 600 |
| TAAGGTTTCA CAGAATGTCC TTGAATCTGT AACAGCTATG GCAGTAGAGG TAGGTTTTTC | 660 |

AGTCCTTGGC TTGGACTTTT CTCCCATCCA AGGTGGACAT GGAAATATTG AATTTTGTAGC 720  
 GTATTTGAAA AAAGAAAAGT CAGCAAGCAA TCAGATTCTT GCTGAGATTA AAGAAGCAGT 780  
 AGAGAGGGCG CATAGTCAAT TAAAAATGA A 811

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 270 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Lys | Glu | Arg | Val | Asp | Val | Leu | Ala | Tyr | Lys | Gln | Gly | Leu | Phe | Glu | 1   | 5   | 10  | 15  |
| Thr | Arg | Glu | Gln | Ala | Lys | Arg | Gly | Val | Met | Ala | Gly | Leu | Val | Val | Ala | 20  | 25  | 30  |     |
| Val | Leu | Asn | Gly | Glu | Arg | Phe | Asp | Lys | Pro | Gly | Glu | Lys | Ile | Pro | Asp | 35  | 40  | 45  |     |
| Asp | Thr | Glu | Leu | Lys | Leu | Lys | Gly | Glu | Lys | Leu | Lys | Tyr | Val | Ser | Arg | 50  | 55  | 60  |     |
| Gly | Gly | Leu | Lys | Leu | Glu | Lys | Ala | Leu | Gln | Val | Phe | Asp | Leu | Ser | Val | 65  | 70  | 75  | 80  |
| Asp | Gly | Ala | Thr | Thr | Ile | Asp | Ile | Gly | Ala | Ser | Thr | Gly | Gly | Phe | Thr | 85  | 90  | 95  |     |
| Asp | Val | Met | Leu | Gln | Asn | Ser | Ala | Lys | Leu | Val | Phe | Ala | Val | Asp | Val | 100 | 105 | 110 |     |
| Gly | Thr | Asn | Gln | Leu | Ala | Trp | Lys | Leu | Arg | Gln | Asp | Pro | Arg | Val | Val | 115 | 120 | 125 |     |
| Ser | Met | Glu | Gln | Phe | Asn | Phe | Arg | Tyr | Ala | Glu | Lys | Thr | Asp | Phe | Glu | 130 | 135 | 140 |     |
| Gln | Glu | Pro | Ser | Phe | Ala | Ser | Ile | Asp | Val | Ser | Phe | Ile | Ser | Leu | Ser | 145 | 150 | 155 | 160 |
| Leu | Ile | Leu | Pro | Ala | Leu | His | Arg | Val | Leu | Ala | Asp | Gln | Gly | Gln | Val | 165 | 170 | 175 |     |
| Val | Ala | Leu | Val | Lys | Pro | Gln | Phe | Glu | Ala | Gly | Arg | Glu | Gln | Ile | Gly | 180 | 185 | 190 |     |
| Lys | Asn | Gly | Ile | Ile | Arg | Asp | Ala | Lys | Val | His | Gln | Asn | Val | Leu | Glu | 195 | 200 | 205 |     |
| Ser | Val | Thr | Ala | Met | Ala | Val | Glu | Val | Gly | Phe | Ser | Val | Leu | Gly | Leu | 210 | 215 | 220 |     |
| Asp | Phe | Ser | Pro | Ile | Gln | Gly | Gly | His | Gly | Asn | Ile | Glu | Phe | Leu | Ala | 225 | 230 | 235 | 240 |

Tyr Leu Lys Lys Glu Lys Ser Ala Ser Asn Gln Ile Leu Ala Glu Ile  
 245 250 255

Lys Glu Ala Val Glu Arg Ala His Ser Gln Phe Lys Asn Glu  
 260 265 270

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| TTGTTCTAT GAACTTGGTC GTCACCAAGC TGGTCAGGTT AAGAAAGAGT CTAATCGAGT  | 60   |
| TTCTTATATA GATGGTGATC AGGCTGGTCA AAAGGCAGAA AACTTGACAC CAGATGAAGT | 120  |
| CAGTAAGAGG GAGGGGATCA ACGCCGAACA AATNGTNATC AAGATTACGG ATCAAGGTTA | 180  |
| TGTGACCTCT CATGGAGACC ATTATCATTA CTATAATGGC AAGGTTCTTT ATGATGCCAT | 240  |
| CATCAGTGAA GAGCTCCTCA TGAAAGATCC GAATTATCAG TTGAAGGATT CAGACATTGT | 300  |
| CAATGAAATC AAGGGTGGTT ATGTCATTAA GGTAACGGT AAATACTATG TNTACCTTAA  | 360  |
| GGATGCAGCT CATGCGGATA ATATTCGGAC AAAAGAAGAG ATTAAACGTC AGAAGCAGGA | 420  |
| ACGCAGTCAT AATCATAACT CAAGAGCAGA TAATGCTGTT GCTGCAGCCA GAGCCCAAGG | 480  |
| ACGTTATACA ACGGATGATG GGTATATCTT CAATGCATCT GATATCATTG AGGACACGGG | 540  |
| TGATGCTTAT ATCGTTCCTC ACGGCGACCA TTACCATTAC ATTCCTAAGA ATGAGTTATC | 600  |
| AGCTAGCGAG TTAGCTGCTG CAGAAGCCTA TTGGAATGGG AAGCAGGGAT CTCGTCCTTC | 660  |
| TTCAAGTTCT AGTTATAATG CAAATCCAGC TCAACCAAGA TTGTCAGAGA ACCACAATCT | 720  |
| GACTGTCACT CCAACTTATC ATCAAAATCA AGGGGAAAC ATTTCAAGCC TTTTACGTGA  | 780  |
| ATTGTATGCT AAACCTTAT CAGAACGCCA TGTGGAATCT GATGGCCTTA TTTTCGACCC  | 840  |
| AGCGCAAATC ACAAGTCGAA CCGCCAGAGG TGTAGCTGTC CCTCATGGTA ACCATTACCA | 900  |
| CTTTATCCCT TATGAACAAA TGTCTGAATT GGAAAAACGA ATTGCTCGTA TTATTCCCCT | 960  |
| TCGTTATCGT TCAAACCATT GGGTACCAGA TTCAAGACCA GAACAACCAA GTCCACAATC | 1020 |
| GACTCCGGAA CCTAGTCCAA GTCCGCAACC TGCACCAAT CCTCAACCAG CTCCAAGCAA  | 1080 |
| TCCAATTGAT GAGAAATTGG TCAAAGAAGC TGTTCGAAAA GTAGGCGATG GTTATGTCTT | 1140 |
| TGAGGAGAAT GGAGTTTCTC GTTATATCCC AGCCAAGGAT CTTTCAGCAG AACAGCAGC  | 1200 |
| AGGCATTGAT AGCAAATGG CCAAGCAGGA AAGTTTATCT CATAAGCTAG GAGCTAAGAA  | 1260 |
| AACTGACCTC CCATCTAGTG ATCGAGAATT TTACAATAAG GCTTATGACT TACTAGCAAG | 1320 |
| AATTCACCAA GATTACTTG ATAATAAAGG TCGACAAGTT GATTTTGAGG CTTTGGATAA  | 1380 |

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CCTGTTGGAA CGACTCAAGG ATGTCNCAAG TGATAAAGTC AAGTTAGTGG ANGATATTCT 1440
TGCCTTCTTA GCTCCGATTC GTCATCCAGA ACGTTTAGGA AAACCAAATG CGCAAATTAC 1500
CTACACTGAT GATGAGATTC AAGTAGCCAA GTTGGCAGGC AAGTACACAA CAGAAGACGG 1560
TTATATCTTT GATCCTCGTG ATATAACCAG TGATGAGGGG GATGCCTATG TAACTCCACA 1620
TATGACCCAT AGCCACTGGA TTAAAAAAGA TAGTTTGTCT GAAGCTGAGA GAGCGGCAGC 1680
CCAGGCTTAT GCTAAAGAGA AAGGTTTGAC CCCTCCTTCG ACAGACCATC AGGATTCAGG 1740
AAATACTGAG GCAAAAGGAG CAGAAGCTAT CTACAACCGC GTGAAAGCAG CTAAGAAGGT 1800
GCCACTTGAT CGTATGCCTT ACAATCTTCA ATATACTGTA GAAGTCAAAA ACGGTAGTTT 1860
AATCATACCT CATTATGACC ATTACCATAA CATCAAATTT GAGTGGTTTG ACGAAGGCCT 1920
TTATGAGGCA CCTAAGGGGT ATACTCTTGA GGATCTTTTG GCGACTGTCA AGTACTATGT 1980
CGAACATCCA AACGAACGTC CGCATTGAGA TAATGGTTTT GGTAACGCTA GCGACCATGT 2040
TCAAAGAAAC AAAAATGGTC AAGCTGATAC CAATCAAACG GAAAAACCAA GCGAGGAGAA 2100
ACCTCAGACA GAAAAACCTG AGGAAGAAAC CCCTCGAGAA GAGAAACCGC AAAGCGAGAA 2160
ACCAGAGTCT CCAAACCAA CAGAGGAACC AGAAGAATCA CCAGAGGAAT CAGAAGAACC 2220
TCAGGTCGAG ACTGAAAAGG TTGAAGAAAA ACTGAGAGAG GCTGAAGATT TACTTGAAAA 2280
AATCCAGGAT 2290

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## (2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 763 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## \* (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys Lys Glu
1           5           10           15
Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
20          25          30
Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
35          40          45
Glu Gln Xaa Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
50          55          60
Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
65          70          75          80
Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp
85          90          95
Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asn

```

| 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Lys | Tyr | Tyr | Val | Tyr | Leu | Lys | Asp | Ala | Ala | His | Ala | Asp | Asn | Ile |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Arg | Thr | Lys | Glu | Glu | Ile | Lys | Arg | Gln | Lys | Gln | Glu | Arg | Ser | His | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| His | Asn | Ser | Arg | Ala | Asp | Asn | Ala | Val | Ala | Ala | Ala | Arg | Ala | Gln | Gly |
|     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Arg | Tyr | Thr | Thr | Asp | Asp | Gly | Tyr | Ile | Phe | Asn | Ala | Ser | Asp | Ile | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Asp | Thr | Gly | Asp | Ala | Tyr | Ile | Val | Pro | His | Gly | Asp | His | Tyr | His |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Ile | Pro | Lys | Asn | Glu | Leu | Ser | Ala | Ser | Glu | Leu | Ala | Ala | Ala | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Tyr | Trp | Asn | Gly | Lys | Gln | Gly | Ser | Arg | Pro | Ser | Ser | Ser | Ser | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Asn | Ala | Asn | Pro | Ala | Gln | Pro | Arg | Leu | Ser | Glu | Asn | His | Asn | Leu |
|     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Thr | Val | Thr | Pro | Thr | Tyr | His | Gln | Asn | Gln | Gly | Glu | Asn | Ile | Ser | Ser |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Leu | Arg | Glu | Leu | Tyr | Ala | Lys | Pro | Leu | Ser | Glu | Arg | His | Val | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Asp | Gly | Leu | Ile | Phe | Asp | Pro | Ala | Gln | Ile | Thr | Ser | Arg | Thr | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Gly | Val | Ala | Val | Pro | His | Gly | Asn | His | Tyr | His | Phe | Ile | Pro | Tyr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Gln | Met | Ser | Glu | Leu | Glu | Lys | Arg | Ile | Ala | Arg | Ile | Ile | Pro | Leu |
|     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |
| Arg | Tyr | Arg | Ser | Asn | His | Trp | Val | Pro | Asp | Ser | Arg | Pro | Glu | Gln | Pro |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser | Pro | Gln | Ser | Thr | Pro | Glu | Pro | Ser | Pro | Ser | Pro | Gln | Pro | Ala | Pro |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Asn | Pro | Gln | Pro | Ala | Pro | Ser | Asn | Pro | Ile | Asp | Glu | Lys | Leu | Val | Lys |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Glu | Ala | Val | Arg | Lys | Val | Gly | Asp | Gly | Tyr | Val | Phe | Glu | Glu | Asn | Gly |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Val | Ser | Arg | Tyr | Ile | Pro | Ala | Lys | Asp | Leu | Ser | Ala | Glu | Thr | Ala | Ala |
|     | 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |
| Gly | Ile | Asp | Ser | Lys | Leu | Ala | Lys | Gln | Glu | Ser | Leu | Ser | His | Lys | Leu |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Gly | Ala | Lys | Lys | Thr | Asp | Leu | Pro | Ser | Ser | Asp | Arg | Glu | Phe | Tyr | Asn |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Lys | Ala | Tyr | Asp | Leu | Leu | Ala | Arg | Ile | His | Gln | Asp | Leu | Leu | Asp | Asn |
|     |     |     | 435 |     |     |     | 440 |     |     |     |     | 445 |     |     |     |

Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg  
 450 455 460  
 Leu Lys Asp Val Xaa Ser Asp Lys Val Lys Leu Val Xaa Asp Ile Leu  
 465 470 475 480  
 Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn  
 485 490 495  
 Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala  
 500 505 510  
 Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile  
 515 520 525  
 Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser  
 530 535 540  
 His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala  
 545 550 555 560  
 Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His  
 565 570 575  
 Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn  
 580 585 590  
 Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn  
 595 600 605  
 Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His  
 610 615 620  
 Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu  
 625 630 635 640  
 Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val  
 645 650 655  
 Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly  
 660 665 670  
 Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala  
 675 680 685  
 Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu  
 690 695 700  
 Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys  
 705 710 715 720  
 Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Ser Pro Glu Glu  
 725 730 735  
 Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys Leu Arg  
 740 745 750  
 Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp  
 755 760

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTATAAGGGT GAATTAGAAA AAGGATACCA ATTTGATGGT TGGGAAATTT CTGGTTTCGA | 60  |
| AGGTAAAAAA GACGCTGGCT ATGTTATTAA TCTATCAAAA GATACCTTTA TAAAACCTGT | 120 |
| ATTCAAGAAA ATAGAGGAGA AAAAGGAGGA AGAAAATAAA CCTACTTTTG ATGTATCGAA | 180 |
| AAAGAAAGAT AACCCACAAG TAAACCATAG TCAATTAAAT GAAAGTCACA GAAAAGAGGA | 240 |
| TTTACAAAGA GAAGAGCATT CACAAAAATC TGATTCAACT AAGGATGTTA CAGCTACAGT | 300 |
| TCTTGATAAA AACAATATCA GTAGTAAATC AACTACTAAC AATCCTAATA AG         | 352 |

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 117 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Tyr | Lys | Gly | Glu | Leu | Glu | Lys | Gly | Tyr | Gln | Phe | Asp | Gly | Trp | Glu | Ile | 1   | 5   | 10  | 15 |
| Ser | Gly | Phe | Glu | Gly | Lys | Lys | Asp | Ala | Gly | Tyr | Val | Ile | Asn | Leu | Ser | 20  | 25  | 30  |    |
| Lys | Asp | Thr | Phe | Ile | Lys | Pro | Val | Phe | Lys | Lys | Ile | Glu | Glu | Lys | Lys | 35  | 40  | 45  |    |
| Glu | Glu | Glu | Asn | Lys | Pro | Thr | Phe | Asp | Val | Ser | Lys | Lys | Lys | Asp | Asn | 50  | 55  | 60  |    |
| Pro | Gln | Val | Asn | His | Ser | Gln | Leu | Asn | Glu | Ser | His | Arg | Lys | Glu | Asp | 65  | 70  | 75  | 80 |
| Leu | Gln | Arg | Glu | Glu | His | Ser | Gln | Lys | Ser | Asp | Ser | Thr | Lys | Asp | Val | 85  | 90  | 95  |    |
| Thr | Ala | Thr | Val | Leu | Asp | Lys | Asn | Asn | Ile | Ser | Ser | Lys | Ser | Thr | Thr | 100 | 105 | 110 |    |
| Asn | Asn | Pro | Asn | Lys |     |     |     |     |     |     |     |     |     |     |     | 115 |     |     |    |

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1312 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GAATGTTTCAG GCTCAAGAAA GTTCAGGAAA TAAATCCAC TTTATCAATG TTCAAGAAGG  | 60   |
| TGGCAGTGAT GCGATTATTC TTGAAAGCAA TGGACATTTT GCCATGGTGG ATACAGGAGA  | 120  |
| AGATTATGAT TTCCCAGATG GAAGTGATTC TCGCTATCCA TGGAGAGAAG GAATTGAAAC  | 180  |
| GTCTTATAAG CATGTTCTAA CAGACCGTGT CTTTCGTCGT TTGAAGGAAT TGGGTGTCCA  | 240  |
| AAACTTGAT TTTATTTTGG TGACCCATAC CCACAGTGAT CATATTGGAA ATGTTGATGA   | 300  |
| ATTACTGTCT ACCTATCCAG TTGACCGAGT CTATCTTAAG AAATATAGTG ATAGTCGTAT  | 360  |
| TACTAATTCT GAACGTCTAT GGGATAATCT GTATGGCTAT GATAAGGTTT TACAGACTGC  | 420  |
| TGCAGAAAAA GGTGTTTCAG TTATTCAAAA TATCACACAA GGGGATGCTC ATTTTCAGTT  | 480  |
| TGGGGACATG GATATTCAGC TCTATAATTA TGAAAATGAA ACTGATTCAT CGGGTGAATT  | 540  |
| AAAGAAAATT TGGGATGACA ATTCCAATTC CTTGATTAGC GTGGTGAAAG TCAATGGCAA  | 600  |
| GAAATTTAC CTTGGGGGCG ATTTAGATAA TGTTTCATGGA GCAGAAGACA AGTATGGTCC  | 660  |
| TCTCATTGGA AAAGTTGATT TGATGAAGTT TAATCATCAC CATGATACCA ACAAATCAAA  | 720  |
| TACCAAGGAT TTCATTAAAA ATTTGAGTCC GAGTTTGATT GTTCAAACCT CGGATAGTCT  | 780  |
| ACCTTGGA AAAATGGTGTG ATAGTGAGTA TGTTAATTGG CTCAAAGAAC GAGGAATTGA   | 840  |
| GAGAAATCAAC GCAGCCAGCA AAGACTATGA TGCAACAGTT TTTGATATTC GAAAAGACGG | 900  |
| TTTTGTCAAT ATTTCAACAT CCTACAAGCC GATTCCAAGT TTTCAAGCTG GTTGGCATAA  | 960  |
| GAGTGCATAT GGGAACTGGT GGTATCAAGC GCCTGATTCT ACAGGAGAGT ATGCTGTCGG  | 1020 |
| TTGGAATGAA ATCGAAGGTG AATGGTATTA CTTTAACCAA ACGGGTATCT TGTTACAGAA  | 1080 |
| TCAATGGAAA AAATGGAACA ATCATTGGTT CTATTTGACA GACTCTGGTG CTTCTGCTAA  | 1140 |
| AAATTGGAAAG AAAATCGCTG GAATCTGGTA TTATTTTAAC AAAGAAAACC AGATGGAAAT | 1200 |
| TGGTTGGATT CAAGATAAAG AGCAGTGGTA TTATTTGGAT GTTGATGGTT CTATGAAGAC  | 1260 |
| AGGATGGCTT CAATATATGG GGCAATGGTA TTACTTTGCT CCATCAGGGG AA          | 1312 |

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 437 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asn Val Gln Ala Gln Glu Ser Ser Gly Asn Lys Ile His Phe Ile Asn

| 1                                                               | 5   | 10  | 15  |
|-----------------------------------------------------------------|-----|-----|-----|
| Val Gln Glu Gly Gly Ser Asp Ala Ile Ile Leu Glu Ser Asn Gly His | 20  | 25  | 30  |
| Phe Ala Met Val Asp Thr Gly Glu Asp Tyr Asp Phe Pro Asp Gly Ser | 35  | 40  | 45  |
| Asp Ser Arg Tyr Pro Trp Arg Glu Gly Ile Glu Thr Ser Tyr Lys His | 50  | 55  | 60  |
| Val Leu Thr Asp Arg Val Phe Arg Arg Leu Lys Glu Leu Gly Val Gln | 65  | 70  | 75  |
| Lys Leu Asp Phe Ile Leu Val Thr His Thr His Ser Asp His Ile Gly | 85  | 90  | 95  |
| Asn Val Asp Glu Leu Leu Ser Thr Tyr Pro Val Asp Arg Val Tyr Leu | 100 | 105 | 110 |
| Lys Lys Tyr Ser Asp Ser Arg Ile Thr Asn Ser Glu Arg Leu Trp Asp | 115 | 120 | 125 |
| Asn Leu Tyr Gly Tyr Asp Lys Val Leu Gln Thr Ala Ala Glu Lys Gly | 130 | 135 | 140 |
| Val Ser Val Ile Gln Asn Ile Thr Gln Gly Asp Ala His Phe Gln Phe | 145 | 150 | 155 |
| Gly Asp Met Asp Ile Gln Leu Tyr Asn Tyr Glu Asn Glu Thr Asp Ser | 165 | 170 | 175 |
| Ser Gly Glu Leu Lys Lys Ile Trp Asp Asp Asn Ser Asn Ser Leu Ile | 180 | 185 | 190 |
| Ser Val Val Lys Val Asn Gly Lys Lys Ile Tyr Leu Gly Gly Asp Leu | 195 | 200 | 205 |
| Asp Asn Val His Gly Ala Glu Asp Lys Tyr Gly Pro Leu Ile Gly Lys | 210 | 215 | 220 |
| Val Asp Leu Met Lys Phe Asn His His His Asp Thr Asn Lys Ser Asn | 225 | 230 | 235 |
| Thr Lys Asp Phe Ile Lys Asn Leu Ser Pro Ser Leu Ile Val Gln Thr | 245 | 250 | 255 |
| Ser Asp Ser Leu Pro Trp Lys Asn Gly Val Asp Ser Glu Tyr Val Asn | 260 | 265 | 270 |
| Trp Leu Lys Glu Arg Gly Ile Glu Arg Ile Asn Ala Ala Ser Lys Asp | 275 | 280 | 285 |
| Tyr Asp Ala Thr Val Phe Asp Ile Arg Lys Asp Gly Phe Val Asn Ile | 290 | 295 | 300 |
| Ser Thr Ser Tyr Lys Pro Ile Pro Ser Phe Gln Ala Gly Trp His Lys | 305 | 310 | 315 |
| Ser Ala Tyr Gly Asn Trp Trp Tyr Gln Ala Pro Asp Ser Thr Gly Glu | 325 | 330 | 335 |
| Tyr Ala Val Gly Trp Asn Glu Ile Glu Gly Glu Trp Tyr Tyr Phe Asn | 340 | 345 | 350 |

Gln Thr Gly Ile Leu Leu Gln Asn Gln Trp Lys Lys Trp Asn Asn His  
           355                                  360                                  365  
 Trp Phe Tyr Leu Thr Asp Ser Gly Ala Ser Ala Lys Asn Trp Lys Lys  
           370                                  375                                  380  
 Ile Ala Gly Ile Trp Tyr Tyr Phe Asn Lys Glu Asn Gln Met Glu Ile  
           385                                  390                                  395                                  400  
 Gly Trp Ile Gln Asp Lys Glu Gln Trp Tyr Tyr Leu Asp Val Asp Gly  
                                   405                                  410                                  415  
 Ser Met Lys Thr Gly Trp Leu Gln Tyr Met Gly Gln Trp Tyr Tyr Phe  
                                   420                                  425                                  430  
 Ala Pro Ser Gly Glu  
                                   435

## (2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1855 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| CTTGGGTGTA ACCCATATCC AGCTCCTTCC AGTCTTGTCT TACTACTTTG TCAATGAATT | 60   |
| GAAAAACCAT GAACGCTTGT CTGACTACGC TTCAAGCAAC AGCAACTACA ACTGGGGATA | 120  |
| TGACCCTCAA AACTACTTCT CCTTGACTGG TATGTACTCA AGCGATCCTA AGAATCCAGA | 180  |
| AAAACGAATC GCAGAATTTA AAAACCTCAT CAACGAAATC CACAAACGTG GTATGGGAGC | 240  |
| TATCCTAGAT GTCGTTTATA ACCACACAGC CAAAGTCGAT CTCTTTGAAG ATTTGGAACC | 300  |
| AAACTACTAC CACTTTATGG ATGCCGATGG CACACCTCGA ACTAGCTTTG GTGGTGGACG | 360  |
| CTTGGGGACA ACCCACCATA TGACCAAACG GCTCCTAATT GACTCTATCA AATACCTAGT | 420  |
| TGATACCTAC AAAGTGGATG GCTTCCGTTT CGATATGATG GGAGACCATG ACGCCGCTTC | 480  |
| TATCGAAGAA GCTTACAAGG CTGCACGCGC CCTCAATCCA AACCTCATCA TGCTTGGTGA | 540  |
| AGGTTGGAGA ACCTATGCCG GTGATGAAAA CATGCCTACT AAAGCTGCTG ACCAAGATTG | 600  |
| GATGAAACAT ACCGATACTG TCGCTGTCTT TTCAGATGAC ATCCGTAACA ACCTCAAATC | 660  |
| TGGTTATCCA AACGAAGGTC AACCTGCCTT TATCACAGGT GGCAAGCGTG ATGTCAACAC | 720  |
| CATCTTTAAA AATCTCATTG CTCAACCAAC TAACTTTGAA GCTGACAGCC CTGGAGATGT | 780  |
| CATCCAATAC ATCGCAGCCC ATGATAACTT GACCCTCTTT GACATCATTG CCCAGTCTAT | 840  |
| CAAAAAAGAC CCAAGCAAGG CTGAGAACTA TGCTGAAATC CACCGTCGTT TACGACTTGG | 900  |
| AAATCTCATG GTCTTGACAG CTCAAGGAAC TCCATTTATC CACTCCGGTC AGGAATATGG | 960  |
| ACGTACTAAA CAATTCCGTG ACCCAGCCTA CAAGACTCCA GTAGCAGAGG ATAAGGTTCC | 1020 |

```

AAACAAATCT CACTTGTTCG GTGATAAGGA CGGCAACCCA TTTGACTATC CTTACTTCAT      1080
CCATGACTCT TACGATTCTA GTGATGCAGT CAACAAGTTT GACTGGACTA AGGCTACAGA      1140
TGGTAAAGCT TATCCTGAAA ATGTCAAGAG CCGTGACTAT ATGAAAGGTT TGATTGCCCT      1200
TCGTCAATCT ACAGATGCCT TCCGACTTAA GAGTCTTCAA GATATCAAAG ACCGTGTCCA      1260
CCTCATCACT GTCCCAGGCC AAAATGGTGT GGAAAAAGAG GATGTAGTGA TTGGCTACCA      1320
AATCACTGCT CCAAACGGCG ATATCTACGC AGTCTTTGTC AATGCGGATG AAAAAGCTCG      1380
CGAATTTAAT TTGGGAACTG CCTTTGCACA TCTAAGAAAT GCGGAAGTTT TGGCAGATGA      1440
AAACCAAGCA GGACCAGTCG GAATTGCCAA CCCGAAAGGA CTTGAATGGA CTGAAAAAGG      1500
CTTGAAATTG AATGCCCTTA CAGCTACTGT TCTTCGAGTC TCTCAAAATG GAACTAGCCA      1560
TGAGTCAACT GCAGAAGAGA AACCAGACTC AACCCTTCC AAGCCTGAAC ATCAAAATGA      1620
AGCTTCTCAC CCTGCACATC AAGACCCAGC TCCAGAAGCT AGACCTGATT CTACTAAACC      1680
AGATGCCAAA GTAGCTGATG CGGAAAATAA ACCTAGCCAA GCTACAGCTG ATTCACAAGC      1740
TGAACAACCA GCACAAGAAG CACAAGCATC ATCTGTAAAA GAAGCGGTTC GAAACGAATC      1800
GGTAGAAAAC TCTAGCAAGG AAAATATACC TGCAACCCCA GATAAACAAG CTGAA          1855

```

## (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 618 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

Leu Gly Val Thr His Ile Gln Leu Leu Pro Val Leu Ser Tyr Tyr Phe
1          5          10          15
Val Asn Glu Leu Lys Asn His Glu Arg Leu Ser Asp Tyr Ala Ser Ser
20          25          30
Asn Ser Asn Tyr Asn Trp Gly Tyr Asp Pro Gln Asn Tyr Phe Ser Leu
35          40          45
Thr Gly Met Tyr Ser Ser Asp Pro Lys Asn Pro Glu Lys Arg Ile Ala
50          55          60
Glu Phe Lys Asn Leu Ile Asn Glu Ile His Lys Arg Gly Met Gly Ala
65          70          75          80
Ile Leu Asp Val Val Tyr Asn His Thr Ala Lys Val Asp Leu Phe Glu
85          90          95
Asp Leu Glu Pro Asn Tyr Tyr His Phe Met Asp Ala Asp Gly Thr Pro
100          105          110
Arg Thr Ser Phe Gly Gly Gly Arg Leu Gly Thr Thr His His Met Thr

```

| 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Arg | Leu | Leu | Ile | Asp | Ser | Ile | Lys | Tyr | Leu | Val | Asp | Thr | Tyr | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Asp | Gly | Phe | Arg | Phe | Asp | Met | Met | Gly | Asp | His | Asp | Ala | Ala | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Glu | Glu | Ala | Tyr | Lys | Ala | Ala | Arg | Ala | Leu | Asn | Pro | Asn | Leu | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Leu | Gly | Glu | Gly | Trp | Arg | Thr | Tyr | Ala | Gly | Asp | Glu | Asn | Met | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Lys | Ala | Ala | Asp | Gln | Asp | Trp | Met | Lys | His | Thr | Asp | Thr | Val | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Phe | Ser | Asp | Asp | Ile | Arg | Asn | Asn | Leu | Lys | Ser | Gly | Tyr | Pro | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Gly | Gln | Pro | Ala | Phe | Ile | Thr | Gly | Gly | Lys | Arg | Asp | Val | Asn | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ile | Phe | Lys | Asn | Leu | Ile | Ala | Gln | Pro | Thr | Asn | Phe | Glu | Ala | Asp | Ser |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Gly | Asp | Val | Ile | Gln | Tyr | Ile | Ala | Ala | His | Asp | Asn | Leu | Thr | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Phe | Asp | Ile | Ile | Ala | Gln | Ser | Ile | Lys | Lys | Asp | Pro | Ser | Lys | Ala | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Tyr | Ala | Glu | Ile | His | Arg | Arg | Leu | Arg | Leu | Gly | Asn | Leu | Met | Val |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Thr | Ala | Gln | Gly | Thr | Pro | Phe | Ile | His | Ser | Gly | Gln | Glu | Tyr | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Arg | Thr | Lys | Gln | Phe | Arg | Asp | Pro | Ala | Tyr | Lys | Thr | Pro | Val | Ala | Glu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asp | Lys | Val | Pro | Asn | Lys | Ser | His | Leu | Leu | Arg | Asp | Lys | Asp | Gly | Asn |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Pro | Phe | Asp | Tyr | Pro | Tyr | Phe | Ile | His | Asp | Ser | Tyr | Asp | Ser | Ser | Asp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ala | Val | Asn | Lys | Phe | Asp | Trp | Thr | Lys | Ala | Thr | Asp | Gly | Lys | Ala | Tyr |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Pro | Glu | Asn | Val | Lys | Ser | Arg | Asp | Tyr | Met | Lys | Gly | Leu | Ile | Ala | Leu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Arg | Gln | Ser | Thr | Asp | Ala | Phe | Arg | Leu | Lys | Ser | Leu | Gln | Asp | Ile | Lys |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Asp | Arg | Val | His | Leu | Ile | Thr | Val | Pro | Gly | Gln | Asn | Gly | Val | Glu | Lys |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Glu | Asp | Val | Val | Ile | Gly | Tyr | Gln | Ile | Thr | Ala | Pro | Asn | Gly | Asp | Ile |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Tyr | Ala | Val | Phe | Val | Asn | Ala | Asp | Glu | Lys | Ala | Arg | Glu | Phe | Asn | Leu |
|     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |

Gly Thr Ala Phe Ala His Leu Arg Asn Ala Glu Val Leu Ala Asp Glu  
 465 470 475 480  
 Asn Gln Ala Gly Pro Val Gly Ile Ala Asn Pro Lys Gly Leu Glu Trp  
 485 490 495  
 Thr Glu Lys Gly Leu Lys Leu Asn Ala Leu Thr Ala Thr Val Leu Arg  
 500 505 510  
 Val Ser Gln Asn Gly Thr Ser His Glu Ser Thr Ala Glu Glu Lys Pro  
 515 520 525  
 Asp Ser Thr Pro Ser Lys Pro Glu His Gln Asn Glu Ala Ser His Pro  
 530 535 540  
 Ala His Gln Asp Pro Ala Pro Glu Ala Arg Pro Asp Ser Thr Lys Pro  
 545 550 555 560  
 Asp Ala Lys Val Ala Asp Ala Glu Asn Lys Pro Ser Gln Ala Thr Ala  
 565 570 575  
 Asp Ser Gln Ala Glu Gln Pro Ala Gln Glu Ala Gln Ala Ser Ser Val  
 580 585 590  
 Lys Glu Ala Val Arg Asn Glu Ser Val Glu Asn Ser Ser Lys Glu Asn  
 595 600 605  
 Ile Pro Ala Thr Pro Asp Lys Gln Ala Glu  
 610 615

## (2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1774 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TAGTGATGGT ACTTGGCAAG GAAAACAGTA TCTGAAAGAA GATGGCAGTC AAGCAGCAAA  | 60  |
| TGAGTGGGTT TTNGATACTC ATTATCAATC TTGGTTCCTAT ATAAAAGCAG ATGCTAACTA | 120 |
| TGCTGAAAAT GAATGGCTAA AGCAAGGTGA CGACTATTTT TACCTCAAAT CTGGTGGCTA  | 180 |
| TATGGCCAAA TCAGAATGGG TAGAAGACAA GGGAGCCTTT TATTATCTTG ACCAAGATGG  | 240 |
| AAAGATGAAA AGAAATGCTT GGGTAGGAAC TTCCTATGTT GGTGCAACAG GTGCCAAAGT  | 300 |
| AATAGAAGAC TGGGTCTATG ATTCTCAATA CGATGCTTGG TTTTATATCA AAGCAGATGG  | 360 |
| ACAGCACGCA GAGAAAGAAT GGCTCCAAAT TAAAGGGAAG GACTATTATT TCAAATCCGG  | 420 |
| TGGTTATCTA CTGACAAGTC AGTGGATTAA TCAAGCTTAT GTGAATGCTA GTGGTGCCAA  | 480 |
| AGTACAGCAA GGTTGGCTTT TTGACAAACA ATACCAATCT TGGTTTTACA TCAAAGAAAA  | 540 |
| TGGAAACTAT GCTGATAAAG AATGGATTTT CGAGAATGGT CACTATTATT ATCTAAAATC  | 600 |
| CGGTGGCTAC ATGGCAGCCA ATGAATGGAT TTGGGATAAG GAATCTTGGT TTTATCTCAA  | 660 |

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ATTTGATGGG AAAATGGCTG AAAAAGAATG GGTCTACGAT TCTCATAGTC AAGCTTGGTA      720
CTACTTCAAA TCCGGTGGTT ACATGACAGC CAATGAATGG ATTTGGGATA AGGAATCTTG      780
GTTTTACCTC AAATCTGATG GGAAAATAGC TGAAAAAGAA TGGGTCTACG ATTCTCATAG      840
TCAAGCTTGG TACTACTTCA AATCTGGTGG CTACATGGCG AAAAATGAGA CAGTAGATGG      900
TTATCAGCTT GGAAGCGATG GTAAATGGCT TGGAGGAAAA ACTACAAATG AAAATGCTGC      960
TTACTATCAA GTAGTGCCTG TTACAGCCAA TGTTTATGAT TCAGATGGTG AAAAGCTTTC     1020
CTATATATCG CAAGGTAGTG TCGTATGGCT AGATAAGGAT AGAAAAAGTG ATGACAAGCG     1080
CTTGGCTATT ACTATTTCTG GTTTGTCAGG CTATATGAAA ACAGAAGATT TACAAGCGCT     1140
AGATGCTAGT AAGGACTTTA TCCCTTATTA TGAGAGTGAT GGCCACCGTT TTTATCACTA     1200
TGTGGCTCAG AATGCTAGTA TCCCAGTAGC TTCTCATCTT TCTGATATGG AAGTAGGCAA     1260
GAAATATTAT TCGGCAGATG GCCTGCATTT TGATGGTTTT AAGCTTGAGA ATCCCTTCCT     1320
TTTCAAAGAT TTAACAGAGG CTACAAACTA CAGTGCTGAA GAATTGGATA AGGTATTTAG     1380
TTTGCTAAAC ATTAACAATA GCCTTTTGGG GAACAAGGGC GCTACTTTTA AGGAAGCCGA     1440
AGAACATTAC CATATCAATG CTCTTTATCT CCTTGCCCAT AGTGCCCTAG AAAGTAACTG     1500
GGGAAGAAGT AAAATTGCCA AAGATAAGAA TAATTCTTTT GGCATTACAG CCTATGATAC     1560
GACCCCTTAC CTTTCTGCTA AGACATTTGA TGATGTGGAT AAGGGAATTT TAGGTGCAAC     1620
CAAGTGGATT AAGGAAAATT ATATCGATAG GGAAGAAGT TTCCTTGGA ACAAGGCTTC     1680
TGGTATGAAT GTGGAATATG CTTACAGACC TTATTGGGGC GAAAAAATTG CTAGTGTGAT     1740
GATGAAAATC AATGAGAAGC TAGGTGGCAA AGAT                                     1774

```

## (2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 591 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

Ser Asp Gly Thr Trp Gln Gly Lys Gln Tyr Leu Lys Glu Asp Gly Ser
1          5          10
Gln Ala Ala Asn Glu Trp Val Xaa Asp Thr His Tyr Gln Ser Trp Phe
          20          25          30
Tyr Ile Lys Ala Asp Ala Asn Tyr Ala Glu Asn Glu Trp Leu Lys Gln
          35          40          45
Gly Asp Asp Tyr Phe Tyr Leu Lys Ser Gly Gly Tyr Met Ala Lys Ser
50          55          60

```

Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp Gln Asp Gly  
 65 70 75 80  
 Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val Gly Ala Thr  
 85 90 95  
 Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln Tyr Asp Ala  
 100 105 110  
 Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys Glu Trp Leu  
 115 120 125  
 Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly Tyr Leu Leu  
 130 135 140  
 Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser Gly Ala Lys  
 145 150 155 160  
 Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser Trp Phe Tyr  
 165 170 175  
 Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile Phe Glu Asn  
 180 185 190  
 Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala Ala Asn Glu  
 195 200 205  
 Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Phe Asp Gly Lys  
 210 215 220  
 Met Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr  
 225 230 235 240  
 Tyr Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp Ile Trp Asp  
 245 250 255  
 Lys Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile Ala Glu Lys  
 260 265 270  
 Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr Phe Lys Ser  
 275 280 285  
 Gly Gly Tyr Met Ala Lys Asn Glu Thr Val Asp Gly Tyr Gln Leu Gly  
 290 295 300  
 Ser Asp Gly Lys Trp Leu Gly Gly Lys Thr Thr Asn Glu Asn Ala Ala  
 305 310 315 320  
 Tyr Tyr Gln Val Val Pro Val Thr Ala Asn Val Tyr Asp Ser Asp Gly  
 325 330 335  
 Glu Lys Leu Ser Tyr Ile Ser Gln Gly Ser Val Val Trp Leu Asp Lys  
 340 345 350  
 Asp Arg Lys Ser Asp Asp Lys Arg Leu Ala Ile Thr Ile Ser Gly Leu  
 355 360 365  
 Ser Gly Tyr Met Lys Thr Glu Asp Leu Gln Ala Leu Asp Ala Ser Lys  
 370 375 380  
 Asp Phe Ile Pro Tyr Tyr Glu Ser Asp Gly His Arg Phe Tyr His Tyr  
 385 390 395 400  
 Val Ala Gln Asn Ala Ser Ile Pro Val Ala Ser His Leu Ser Asp Met

|                                                                 |                     |                                 |     |     |     |
|-----------------------------------------------------------------|---------------------|---------------------------------|-----|-----|-----|
|                                                                 | 405                 |                                 | 410 |     | 415 |
| Glu Val Gly                                                     | Lys Lys Tyr Tyr Ser | Ala Asp Gly Leu His Phe Asp Gly |     |     |     |
|                                                                 | 420                 | 425                             |     | 430 |     |
| Phe Lys Leu Glu Asn Pro Phe Leu Phe Lys Asp Leu Thr Glu Ala Thr |                     |                                 |     |     |     |
|                                                                 | 435                 | 440                             |     | 445 |     |
| Asn Tyr Ser Ala Glu Glu Leu Asp Lys Val Phe Ser Leu Leu Asn Ile |                     |                                 |     |     |     |
|                                                                 | 450                 | 455                             |     | 460 |     |
| Asn Asn Ser Leu Leu Glu Asn Lys Gly Ala Thr Phe Lys Glu Ala Glu |                     |                                 |     |     |     |
|                                                                 | 465                 | 470                             |     | 475 | 480 |
| Glu His Tyr His Ile Asn Ala Leu Tyr Leu Leu Ala His Ser Ala Leu |                     |                                 |     |     |     |
|                                                                 | 485                 |                                 | 490 |     | 495 |
| Glu Ser Asn Trp Gly Arg Ser Lys Ile Ala Lys Asp Lys Asn Asn Phe |                     |                                 |     |     |     |
|                                                                 | 500                 | 505                             |     | 510 |     |
| Phe Gly Ile Thr Ala Tyr Asp Thr Thr Pro Tyr Leu Ser Ala Lys Thr |                     |                                 |     |     |     |
|                                                                 | 515                 | 520                             |     | 525 |     |
| Phe Asp Asp Val Asp Lys Gly Ile Leu Gly Ala Thr Lys Trp Ile Lys |                     |                                 |     |     |     |
|                                                                 | 530                 | 535                             |     | 540 |     |
| Glu Asn Tyr Ile Asp Arg Gly Arg Thr Phe Leu Gly Asn Lys Ala Ser |                     |                                 |     |     |     |
|                                                                 | 545                 | 550                             |     | 555 | 560 |
| Gly Met Asn Val Glu Tyr Ala Ser Asp Pro Tyr Trp Gly Glu Lys Ile |                     |                                 |     |     |     |
|                                                                 | 565                 | 570                             |     | 575 |     |
| Ala Ser Val Met Met Lys Ile Asn Glu Lys Leu Gly Gly Lys Asp     |                     |                                 |     |     |     |
|                                                                 | 580                 | 585                             |     | 590 |     |

## (2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1105 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TGGGATTCAA TATGTCAGAG ATGATACTAG AGATAAAGAA GAGGGAATAG AGTATGATGA | 60  |
| CGCTGACAAT GGGGATATTA TTGTAAAAGT AGCGACTAAA CCTAAGGTAG TAACCAAGAA | 120 |
| AATTTCAAGT ACGCGAATTC GTTATGAAAA AGATGAAACA AAAGACCGTA GTGAAAATCC | 180 |
| TGTTACAATT GATGGAGAGG ATGGCTATGT AACTACGACA AGGACCTACG ATGTTAATCC | 240 |
| AGAGACTGGT TATGTTACCG AACAGGTTAC TGTTGATAGA AAAGAAGCCA CGGATACAGT | 300 |
| TATCAAAGTT CCAGCTAAAA GCAAGGTTGA AGAAGTTCTT GTTCCATTTG CTAATAAATA | 360 |
| TGAAGCAGAC AATGACCTTT CTGCAGGACA GGAGCAAGAG ATTACTCTAG GAAAGAATGG | 420 |
| GAAAACAGTT ACAACGATAA CTTATAATGT AGATGGAAAG AGTGGACAAG TAACTGAGAG | 480 |
| TACTTTAAGT CAAAAAAG ACTCtCAAAC AAGAGTTGTT AAAAAAGaA CCArkCCCCA    | 540 |

```

AGTTCTTGTC CAAGAAATTC CAATCGAAAC AGAATATCTC GATGGCCCaA CTCTTGATAA      600
AaGTCAAGAA GTAGAAGAAG TAGGAGAAAT TGGTAAATTA CTCTTACTAC AATCTATACT      660
GGTAGATGAA CGTGATGGAA CAATTGAAGA AACTACTTCT CGTCAAATTA CTAAAGAGAT      720
GGTAAAAAGA CGTATAAGGA GAGGGACGAG AGAACCTGAA AAAGTTGTTG TTCCTGAGCA      780
ATCATCTATT CCTTCGTATC CTGTATCTGT TACATCTAAC CAAGGAACAG ATGTAGCAGT      840
AGAACCAGCT AAAGCAGTTG CTCCAACAAC AGACTGGAAA CAAGAAAATG GTATGTGGTA      900
TTTTTATAAT ACTGATGGTT CCATGGCAAC AGGTTGGGTA CAAGTTAATA GTTCATGGTA      960
CTACCTCAAC AGCAACGGTT CTATGAAAGT CAATCAATGG TTCCAAGTTG GTGGTAAATG     1020
GTATTATGTA AATACATCGG GTGAGTTAGC GGTCAATACA AGTATAGATG GCTATAGAGT     1080
CAATGATAAT GGTGAATGGG TGCCT   1105

```

## (2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 368 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

Gly Ile Gln Tyr Val Arg Asp Asp Thr Arg Asp Lys Glu Glu Gly Ile
1           5           10           15
Glu Tyr Asp Asp Ala Asp Asn Gly Asp Ile Ile Val Lys Val Ala Thr
20          25          30
Lys Pro Lys Val Val Thr Lys Lys Ile Ser Ser Thr Arg Ile Arg Tyr
35          40          45
Glu Lys Asp Glu Thr Lys Asp Arg Ser Glu Asn Pro Val Thr Ile Asp
50          55          60
Gly Glu Asp Gly Tyr Val Thr Thr Thr Arg Thr Tyr Asp Val Asn Pro
65          70          75          80
Glu Thr Gly Tyr Val Thr Glu Gln Val Thr Val Asp Arg Lys Glu Ala
85          90          95
Thr Asp Thr Val Ile Lys Val Pro Ala Lys Ser Lys Val Glu Glu Val
100         105         110
Leu Val Pro Phe Ala Thr Lys Tyr Glu Ala Asp Asn Asp Leu Ser Ala
115         120         125
Gly Gln Glu Gln Glu Ile Thr Leu Gly Lys Asn Gly Lys Thr Val Thr
130         135         140
Thr Ile Thr Tyr Asn Val Asp Gly Lys Ser Gly Gln Val Thr Glu Ser
145         150         155         160

```

Thr Leu Ser Gln Lys Lys Asp Ser Gln Thr Arg Val Val Lys Lys Arg  
 165 170 175  
 Thr Xaa Pro Gln Val Leu Val Gln Glu Ile Pro Ile Glu Thr Glu Tyr  
 180 185 190  
 Leu Asp Gly Pro Thr Leu Asp Lys Ser Gln Glu Val Glu Glu Val Gly  
 195 200 205  
 Glu Ile Gly Lys Leu Leu Leu Leu Gln Ser Ile Leu Val Asp Glu Arg  
 210 215 220  
 Asp Gly Thr Ile Glu Glu Thr Thr Ser Arg Gln Ile Thr Lys Glu Met  
 225 230 235 240  
 Val Lys Arg Arg Ile Arg Arg Gly Thr Arg Glu Pro Glu Lys Val Val  
 245 250 255  
 Val Pro Glu Gln Ser Ser Ile Pro Ser Tyr Pro Val Ser Val Thr Ser  
 260 265 270  
 Asn Gln Gly Thr Asp Val Ala Val Glu Pro Ala Lys Ala Val Ala Pro  
 275 280 285  
 Thr Thr Asp Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr  
 290 295 300  
 Asp Gly Ser Met Ala Thr Gly Trp Val Gln Val Asn Ser Ser Trp Tyr  
 305 310 315 320  
 Tyr Leu Asn Ser Asn Gly Ser Met Lys Val Asn Gln Trp Phe Gln Val  
 325 330 335  
 Gly Gly Lys Trp Tyr Tyr Val Asn Thr Ser Gly Glu Leu Ala Val Asn  
 340 345 350  
 Thr Ser Ile Asp Gly Tyr Arg Val Asn Asp Asn Gly Glu Trp Val Arg  
 355 360 365

## (2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 661 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGATAATAGA GAAGCATTAA AAACCTTTAT GACGGGTGAA AATTTTTATC TCCAACATTA | 60  |
| TCTAGGAGCA CATAGGGAAG AACTAAATGG AGAGCATGGC TATACCTTCC GTGTTTGGGC | 120 |
| ACCTAATGCT CAGGCTGTTC ACTTGTTGG TGATTTTACC AACTGGATTG AAAATCAGAT  | 180 |
| TCCAATGGTA AGAAATGATT TTGGGGTCTG GGAAGTCTTT ACCAATATGG CTCAAGAAGG | 240 |
| GCATATTTAC AAATATCATG TCACACGTCA AAATGGTCAT CAACTGATGA AGATTGACCC | 300 |
| TTTTGCTGTC AGGTATGAGG CTCGTCCAGG AACAGGGGCA ATCGTAACAG AGCTTCCTGA | 360 |
| GAAGAAATGG AAGGATGGAC TTTGGCTGGC ACGAAGAAAA CGTTGGGGCT TTGAAGAGCG | 420 |

TCCTGTCAAT ATTTATGAAG TTCACGCTGG ATCATGGAAA AGAAATTCTG ATGGCAGTCC 480  
 TTATAGTTTT GCCCAGCTCA AGGATGAACT CATTCTTAT CTCGTTGAAA TGAACATAC 540  
 TCATATTGAG TTTATGCCCT TGATGTCCCA TCCTTTGGGC TTGAGTTGGG GGTATCAGCT 600  
 TATGGGTTAC TTCGCTTTAG AGCATGCTTA TGGCCGACCA GAGGAGTTTC AAGATTTTGT 660  
 C 661

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 220 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Asn | Arg | Glu | Ala | Leu | Lys | Thr | Phe | Met | Thr | Gly | Glu | Asn | Phe | Tyr | 1   | 5   | 10  | 15  |
| Leu | Gln | His | Tyr | Leu | Gly | Ala | His | Arg | Glu | Glu | Leu | Asn | Gly | Glu | His | 20  | 25  | 30  |     |
| Gly | Tyr | Thr | Phe | Arg | Val | Trp | Ala | Pro | Asn | Ala | Gln | Ala | Val | His | Leu | 35  | 40  | 45  |     |
| Val | Gly | Asp | Phe | Thr | Asn | Trp | Ile | Glu | Asn | Gln | Ile | Pro | Met | Val | Arg | 50  | 55  | 60  |     |
| Asn | Asp | Phe | Gly | Val | Trp | Glu | Val | Phe | Thr | Asn | Met | Ala | Gln | Glu | Gly | 65  | 70  | 75  | 80  |
| His | Ile | Tyr | Lys | Tyr | His | Val | Thr | Arg | Gln | Asn | Gly | His | Gln | Leu | Met | 85  | 90  | 95  |     |
| Lys | Ile | Asp | Pro | Phe | Ala | Val | Arg | Tyr | Glu | Ala | Arg | Pro | Gly | Thr | Gly | 100 | 105 | 110 |     |
| Ala | Ile | Val | Thr | Glu | Leu | Pro | Glu | Lys | Lys | Trp | Lys | Asp | Gly | Leu | Trp | 115 | 120 | 125 |     |
| Leu | Ala | Arg | Arg | Lys | Arg | Trp | Gly | Phe | Glu | Glu | Arg | Pro | Val | Asn | Ile | 130 | 135 | 140 |     |
| Tyr | Glu | Val | His | Ala | Gly | Ser | Trp | Lys | Arg | Asn | Ser | Asp | Gly | Ser | Pro | 145 | 150 | 155 | 160 |
| Tyr | Ser | Phe | Ala | Gln | Leu | Lys | Asp | Glu | Leu | Ile | Pro | Tyr | Leu | Val | Glu | 165 | 170 | 175 |     |
| Met | Asn | Tyr | Thr | His | Ile | Glu | Phe | Met | Pro | Leu | Met | Ser | His | Pro | Leu | 180 | 185 | 190 |     |
| Gly | Leu | Ser | Trp | Gly | Tyr | Gln | Leu | Met | Gly | Tyr | Phe | Ala | Leu | Glu | His | 195 | 200 | 205 |     |
| Ala | Tyr | Gly | Arg | Pro | Glu | Glu | Phe | Gln | Asp | Phe | Val |     |     |     |     |     |     |     |     |

210

215

220

## (2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 976 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| AGATTTTGTC GAGGAGTGTC ATACCCATAA TATTGGGGTT ATTGTGGACT GGGTACCAGN  | 60  |
| TCACTTTACC ATCAACGATG ATGCCTTAGC CTATTATGAT GGGACACCGA CTTTGAATA   | 120 |
| CCAAGACCAT AATAAGGCTC ATAACCATGG TTGGGGTGCC CTTAATTTTG ACCTTGAAAA  | 180 |
| AAATGAAGTC CAGTCCTTCT TAATTTCTTG CATTAAGCAT TGGATTGATG TCTATCATT   | 240 |
| GGATGGTATT CGTGTGGATG CTGTTAGCAA CATGCTCTAT TTGGACTATG ATGATGCTCC  | 300 |
| ATGGACACCT AATAAAGATG GCGGAAATCT CAACTATGAA GGTTATTATT TCCTTCAGCG  | 360 |
| CTTGAATGAG GTTATTAAGT TAGAATATCC AGATGTGATG ATGATTGCAG AAGAAAGTTC  | 420 |
| GTCTGCGATC AAGATTACGG GAATGAAAGA GATTGGTGGT CTAGGATTTG ACTACAAATG  | 480 |
| GAACATGGGC TGGATGAATG ATATCCTCCG TTTCTACGAA GAAGATCCGA TCTATCGTAA  | 540 |
| ATATGACTTT AACCTGGTGA CTTTCAGCTT TATGTATGTT TNCAAGGAGA ATTATCTCTT  | 600 |
| GCCATTCTCG CACGATGAAG TGGTTCATGG CAAGAAGAGT ATGATGCATA AGATGTGGGG  | 660 |
| AGATCGTTAC AATCAATTCG CAGGCTTGCG CAATCTCTAT ACGTACCAAA TTTGTCACCC  | 720 |
| TGGTAAGAAA TTGCTCTTCA TGGGTAGCGA ATACGGTCAA TTCCTAGAAT GGAAATCTGA  | 780 |
| AGAACAGTTG GAATGGTCTA ACCTAGAAGA CCCAATGAAT GCTAAGATGA AGTATTTTCGC | 840 |
| TTCTCAGCTA AACCAGTTTT ACAAAGATCA TCGCTGTCTG TGGGAAATTG ATACCAGCTA  | 900 |
| TGATGGTATT GAAATCATTG ATGCGGATAA TCGAGACCAG AGTGTCTCTT CCTTTATTCG  | 960 |
| TAAGGGTAAA AAGGGA                                                  | 976 |

## (2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 325 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Phe | Val | Glu | Glu | Cys | His | Thr | His | Asn | Ile | Gly | Val | Ile | Val | Asp |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |

Trp Val Pro Xaa His Phe Thr Ile Asn Asp Asp Ala Leu Ala Tyr Tyr  
 20 25 30  
 Asp Gly Thr Pro Thr Phe Glu Tyr Gln Asp His Asn Lys Ala His Asn  
 35 40 45  
 His Gly Trp Gly Ala Leu Asn Phe Asp Leu Gly Lys Asn Glu Val Gln  
 50 55 60  
 Ser Phe Leu Ile Ser Cys Ile Lys His Trp Ile Asp Val Tyr His Leu  
 65 70 75 80  
 Asp Gly Ile Arg Val Asp Ala Val Ser Asn Met Leu Tyr Leu Asp Tyr  
 85 90 95  
 Asp Asp Ala Pro Trp Thr Pro Asn Lys Asp Gly Gly Asn Leu Asn Tyr  
 100 105 110  
 Glu Gly Tyr Tyr Phe Leu Gln Arg Leu Asn Glu Val Ile Lys Leu Glu  
 115 120 125  
 Tyr Pro Asp Val Met Met Ile Ala Glu Glu Ser Ser Ser Ala Ile Lys  
 130 135 140  
 Ile Thr Gly Met Lys Glu Ile Gly Gly Leu Gly Phe Asp Tyr Lys Trp  
 145 150 155 160  
 Asn Met Gly Trp Met Asn Asp Ile Leu Arg Phe Tyr Glu Glu Asp Pro  
 165 170 175  
 Ile Tyr Arg Lys Tyr Asp Phe Asn Leu Val Thr Phe Ser Phe Met Tyr  
 180 185 190  
 Val Xaa Lys Glu Asn Tyr Leu Leu Pro Phe Ser His Asp Glu Val Val  
 195 200 205  
 His Gly Lys Lys Ser Met Met His Lys Met Trp Gly Asp Arg Tyr Asn  
 210 215 220  
 Gln Phe Ala Gly Leu Arg Asn Leu Tyr Thr Tyr Gln Ile Cys His Pro  
 225 230 235 240  
 Gly Lys Lys Leu Leu Phe Met Gly Ser Glu Tyr Gly Gln Phe Leu Glu  
 245 250 255  
 Trp Lys Ser Glu Glu Gln Leu Glu Trp Ser Asn Leu Glu Asp Pro Met  
 260 265 270  
 Asn Ala Lys Met Lys Tyr Phe Ala Ser Gln Leu Asn Gln Phe Tyr Lys  
 275 280 285  
 Asp His Arg Cys Leu Trp Glu Ile Asp Thr Ser Tyr Asp Gly Ile Glu  
 290 295 300  
 Ile Ile Asp Ala Asp Asn Arg Asp Gln Ser Val Leu Ser Phe Ile Arg  
 305 310 315 320  
 Lys Gly Lys Lys Gly  
 325

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2134 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ATCTGTAGTT TATGCGGATG AAACACTTAT TACTCATACT GCTGAGAAAC CTAAAGAGGA  | 60   |
| AAAAATGATA GTAGAAGAAA AGGCTGATAA AGCTTTGGAA ACTAAAAATA TAGTTGAAAG  | 120  |
| GACAGAACAA AGTGAACCTA GTTCAACTGA GGCTATTGCA TCTGAGNAGA AAGAAGATGA  | 180  |
| AGCCGTAACCT CCAAAAGAGG AAAAAGTGTC TGCTAAACCG GAAGAAAAAG CTCCAAGGAT | 240  |
| AGAATCACAA GCTTCAAATC AAGAAAAACC GCTCAAGGAA GATGCTAAAG CTGTAACAAA  | 300  |
| TGAAGAAGTG AATCAAATGA TTGAAGACAG GAAAGTGGAT TTTAATCAAA ATTGGTACTT  | 360  |
| TAAACTCAAT GCAAATTCTA AGGAAGCCAT TAAACCTGAT GCAGACGTAT CTACGTGGAA  | 420  |
| AAAATTAGAT TTACCGTATG ACTGGAGTAT CTTTAACGAT TTCGATCATG AATCTCCTGC  | 480  |
| ACAAAATGAA GGTGGACAGC TCAACGGTGG GGAAGCTTGG TATCGCAAGA CTTTCAAACCT | 540  |
| AGATGAAAAA GACCTCAAGA AAAATGTTTCG CCTTACTTTT GATGGCGTCT ACATGGATTC | 600  |
| TCAAGTTTAT GTCAATGGTC AGTTAGTGGG GCATTATCCA AATGGTTATA ACCAGTTCTC  | 660  |
| ATATGATATC ACCAAATACC TTCAAAAAGA TGGTCGTGAG AATGTGATTG CTGTCCATGC  | 720  |
| AGTCAACAAA CAGCCAAGTA GCCGTTGGTA TTCAGGAAGT GGTATCTATC GTGATGTGAC  | 780  |
| TTTACAAGTG ACAGATAAGG TGCATGTTGA GAAAAATGGG ACAACTATTT TAACACCAAA  | 840  |
| ACTTGAAGAA CAACAACATG GCAAGGTTGA AACTCATGTG ACCAGCAAAA TCGTCAATAC  | 900  |
| GGACGACAAA GACCATGAAC TTGTAGCCGA ATATCAAATC GTTGAACGAG GTGGTCATGC  | 960  |
| TGTAACAGGC TTAGTTTCGTA CAGCGAGTCG TACCTTAAAA GCACATGAAT CAACAAGCCT | 1020 |
| AGATGCGATT TTAGAAGTTG AAAGACCAAA ACTCTGGACT GTTTTAAATG ACAAACCTGC  | 1080 |
| CTTGTACGAA TTGATTACGC GTGTTTACCG TGACGGTCAA TTGGTTGATG CTAAGAAGGA  | 1140 |
| TTTGTTTGGT TACCGTTACT ATCACTGGAC TCCAAATGAA GGTTTCTCTT TGAATGGTGA  | 1200 |
| ACGTATTAAA TTCCATGGAG TATCCTTGCA CCACGACCAT GGGGCGCTTG GAGCAGAAGA  | 1260 |
| AAACTATAAA GCAGAATATC GCCGTCTCAA ACAAATGAAG GAGATGGGAG TTAACCTCAT  | 1320 |
| CCGTACAACC CACAACCCTG CTAGTGAGCA AACCTTGCAA ATCGCAGCAG AACTAGGTTT  | 1380 |
| ACTCGTTTCAG GAAGAGGCCT TTGATACGTG GTATGGTGGC AAGAAACCTT ATGACTATGG | 1440 |
| ACGTTTCTTT GAAAAAGATG CCACTCACCC AGAAGCTCGA AAAGGTGAAA AATGGTCTGA  | 1500 |
| TTTTGACCTA CGTACCATGG TCGAAAGAGG CAAAAACAAC CCTGCTATCT TCATGTGGTC  | 1560 |
| AATTGGTAAT GAAATAGGTG AAGCTAATGG TGATGCCCCAC TCTTTAGCAA CTGTTAAACG | 1620 |
| TTTGGTTAAG GTTATCAAGG ATGTTGATAA GACTCGCTAT GTTACCATGG GAGCAGATAA  | 1680 |

ATTCCGTTTC GGTAATGGTA GCGGAGGGCA TGAGAAAATT GCTGATGAAC TCGATGCTGT 1740  
 TGGATTTAAC TATTCTGAAG ATAATTACAA AGCCCTTAGA GCTAAGCATC CAAAATGGTT 1800  
 GATTATATGGA TCAGAAACAT CTTACAGCTAC CCGTACACGT GGAAGTTACT ATCGCCCTGA 1860  
 ACGTGAATTG AAACATAGCA ATGGACCTGA GCGTAATTAT GAACAGTCAG ATTATGGAAA 1920  
 TGATCGTGTG GGTGGGGGA AAACAGCAAC CGCTTCATGG ACTTTTGACC GTGACAACGC 1980  
 TGGCTATGCT GGACAGTTTA TCTGGACAGG TACGGACTAT ATTGGTGAAC CTACACCATG 2040  
 GCACAACCAA AATCAAATC CTGTTAAGAG CTCTTACTTT GGTATCGTAG ATACAGCCGG 2100  
 CATTCCAAA CATGACTTCT ATCTCTACCA AAGC 2134

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 711 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ser Val Val Tyr Ala Asp Glu Thr Leu Ile Thr His Thr Ala Glu Lys  
 1 5 10 15  
 Pro Lys Glu Glu Lys Met Ile Val Glu Glu Lys Ala Asp Lys Ala Leu  
 20 25 30  
 Glu Thr Lys Asn Ile Val Glu Arg Thr Glu Gln Ser Glu Pro Ser Ser  
 35 40 45  
 Thr Glu Ala Ile Ala Ser Glu Xaa Lys Glu Asp Glu Ala Val Thr Pro  
 50 55 60  
 Lys Glu Glu Lys Val Ser Ala Lys Pro Glu Glu Lys Ala Pro Arg Ile  
 65 70 75 80  
 Glu Ser Gln Ala Ser Asn Gln Glu Lys Pro Leu Lys Glu Asp Ala Lys  
 85 90 95  
 Ala Val Thr Asn Glu Glu Val Asn Gln Met Ile Glu Asp Arg Lys Val  
 100 105 110  
 Asp Phe Asn Gln Asn Trp Tyr Phe Lys Leu Asn Ala Asn Ser Lys Glu  
 115 120 125  
 Ala Ile Lys Pro Asp Ala Asp Val Ser Thr Trp Lys Lys Leu Asp Leu  
 130 135 140  
 Pro Tyr Asp Trp Ser Ile Phe Asn Asp Phe Asp His Glu Ser Pro Ala  
 145 150 155 160  
 Gln Asn Glu Gly Gly Gln Leu Asn Gly Gly Glu Ala Trp Tyr Arg Lys  
 165 170 175  
 Thr Phe Lys Leu Asp Glu Lys Asp Leu Lys Lys Asn Val Arg Leu Thr  
 180 185 190

Phe Asp Gly Val Tyr Met Asp Ser Gln Val Tyr Val Asn Gly Gln Leu  
 195 200 205  
 Val Gly His Tyr Pro Asn Gly Tyr Asn Gln Phe Ser Tyr Asp Ile Thr  
 210 215 220  
 Lys Tyr Leu Gln Lys Asp Gly Arg Glu Asn Val Ile Ala Val His Ala  
 225 230 235 240  
 Val Asn Lys Gln Pro Ser Ser Arg Trp Tyr Ser Gly Ser Gly Ile Tyr  
 245 250 255  
 Arg Asp Val Thr Leu Gln Val Thr Asp Lys Val His Val Glu Lys Asn  
 260 265 270  
 Gly Thr Thr Ile Leu Thr Pro Lys Leu Glu Glu Gln Gln His Gly Lys  
 275 280 285  
 Val Glu Thr His Val Thr Ser Lys Ile Val Asn Thr Asp Asp Lys Asp  
 290 295 300  
 His Glu Leu Val Ala Glu Tyr Gln Ile Val Glu Arg Gly Gly His Ala  
 305 310 315 320  
 Val Thr Gly Leu Val Arg Thr Ala Ser Arg Thr Leu Lys Ala His Glu  
 325 330 335  
 Ser Thr Ser Leu Asp Ala Ile Leu Glu Val Glu Arg Pro Lys Leu Trp  
 340 345 350  
 Thr Val Leu Asn Asp Lys Pro Ala Leu Tyr Glu Leu Ile Thr Arg Val  
 355 360 365  
 Tyr Arg Asp Gly Gln Leu Val Asp Ala Lys Lys Asp Leu Phe Gly Tyr  
 370 375 380  
 Arg Tyr Tyr His Trp Thr Pro Asn Glu Gly Phe Ser Leu Asn Gly Glu  
 385 390 395 400  
 Arg Ile Lys Phe His Gly Val Ser Leu His His Asp His Gly Ala Leu  
 405 410 415  
 Gly Ala Glu Glu Asn Tyr Lys Ala Glu Tyr Arg Arg Leu Lys Gln Met  
 420 425 430  
 Lys Glu Met Gly Val Asn Ser Ile Arg Thr Thr His Asn Pro Ala Ser  
 435 440 445  
 Glu Gln Thr Leu Gln Ile Ala Ala Glu Leu Gly Leu Leu Val Gln Glu  
 450 455 460  
 Glu Ala Phe Asp Thr Trp Tyr Gly Gly Lys Lys Pro Tyr Asp Tyr Gly  
 465 470 475 480  
 Arg Phe Phe Glu Lys Asp Ala Thr His Pro Glu Ala Arg Lys Gly Glu  
 485 490 495  
 Lys Trp Ser Asp Phe Asp Leu Arg Thr Met Val Glu Arg Gly Lys Asn  
 500 505 510  
 Asn Pro Ala Ile Phe Met Trp Ser Ile Gly Asn Glu Ile Gly Glu Ala  
 515 520 525

Asn Gly Asp Ala His Ser Leu Ala Thr Val Lys Arg Leu Val Lys Val  
 530 535 540  
 Ile Lys Asp Val Asp Lys Thr Arg Tyr Val Thr Met Gly Ala Asp Lys  
 545 550 555 560  
 Phe Arg Phe Gly Asn Gly Ser Gly Gly His Glu Lys Ile Ala Asp Glu  
 565 570 575  
 Leu Asp Ala Val Gly Phe Asn Tyr Ser Glu Asp Asn Tyr Lys Ala Leu  
 580 585 590  
 Arg Ala Lys His Pro Lys Trp Leu Ile Tyr Gly Ser Glu Thr Ser Ser  
 595 600 605  
 Ala Thr Arg Thr Arg Gly Ser Tyr Tyr Arg Pro Glu Arg Glu Leu Lys  
 610 615 620  
 His Ser Asn Gly Pro Glu Arg Asn Tyr Glu Gln Ser Asp Tyr Gly Asn  
 625 630 635 640  
 Asp Arg Val Gly Trp Gly Lys Thr Ala Thr Ala Ser Trp Thr Phe Asp  
 645 650 655  
 Arg Asp Asn Ala Gly Tyr Ala Gly Gln Phe Ile Trp Thr Gly Thr Asp  
 660 665 670  
 Tyr Ile Gly Glu Pro Thr Pro Trp His Asn Gln Asn Gln Thr Pro Val  
 675 680 685  
 Lys Ser Ser Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His  
 690 695 700  
 Asp Phe Tyr Leu Tyr Gln Ser  
 705 710

## (2) INFORMATION FOR SEQ ID NO: 83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTACTTTGGT ATCGTAGATA CAGCCGGCAT TCCAAAACAT GACTTCTATC TCTACCAAAG  | 60  |
| CCAATGGGTT TCTGTTAAGA AGAAACCGAT GGTACACCTT CTTCTCACT GGAAGTGGGA   | 120 |
| AAACAAAGAA TTAGCATCCA AAGTAGCTGA CTCAGAAGGT AAGATTCCAG TTCGTGCTTA  | 180 |
| TTCGAATGCT TCTAGTGTAG AATTGTTCTT GAATGGAAAA TCTCTTGGTC TTAAGACTTT  | 240 |
| CAATAAAAAA CAAACCAGCG ATGGGCGGAC TTACCAAGAA GGTGCAAATG CTAATGAACT  | 300 |
| TTATCTTGAA TGGAAAGTTG CCTATCAACC AGGTACCTTG GAAGCAATTG CTCGTGATGA  | 360 |
| ATCTGGCAAG GAAATTGCTC GAGATAAGAT TACGACTGCT GGTAAGCCAG CGGCAGTTCTG | 420 |
| TCTTATTAAG GAAGACCATG CGATTGCAGC AGATGGAAAA GACTTGACTT ACATCTACTA  | 480 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TGAAATTGTT GACAGCCAGG GGAATGTGGT TCCAACTGCT AATAATCTGG TTCGCTTCCA  | 540  |
| ATTGCATGGC CAAGGTCAAC TGGTCGGTGT AGATAACGGA GAACAAGCCA GCCGTGAACG  | 600  |
| CTATAAGGCG CAAGCAGATG GTTCTTGGAT TCGTAAAGCA TTTAATGGTA AAGGTGTTGC  | 660  |
| CATTGTCAAA TCAACTGAAC AAGCAGGGAA ATTCACCCTG ACTGCCCCACT CTGATCTCTT | 720  |
| GAAATCGAAC CAAGTCACTG TCTTTACTGG TAAGAAAGAA GGACAAGAGA AGACTGTTTTT | 780  |
| GGGGACAGAA GTGCCAAAAG TACAGACCAT TATTGGAGAG GCACCTGAAA TGCCTACCAC  | 840  |
| TGTTCCGTTT GTATACAGTG ATGGTAGCCG TGCAGAACGT CCTGTAACCT GGTCTTCAGT  | 900  |
| AGATGTGAGC AAGCCTGGTA TTGTAACGGT GAAAGGTATG GCTGACGGAC GAGAAGTAGA  | 960  |
| AGCTCGTGTA GAAGTGATTG CTCTTAAATC AGAGCTACCA GTTGTGAAAC GTATTGCTCC  | 1020 |
| AAATACTGAC TTGAATTCTG TAGACAAATC TGTTTCCTAT GTTTTGATTG ATGGAAGTGT  | 1080 |
| TGAAGAGTAT GAAGTGGACA AGTGGGAGAT TGCCGAAGAA GATAAAGCTA AGTTAGCAAT  | 1140 |
| TCCAGGTTCT CGTATTCAAG CGACCGGTTA TTTAGAAGGT CAACCAATTC ATGCAACCCT  | 1200 |
| TGTGGTAGAA GAAGGCAATC CTGCGGCACC TGCAGTACCA ACTGTAACGG TTGGTGGTGA  | 1260 |
| GGCAGTAACA GGTCTTACTA GTCAAAAACC AATGCAATAC CGCACTCTTG CTTATGGAGC  | 1320 |
| TAAGTTGCCA GAAGTCACAG CAAGTGCTAA AAATGCAGCT GTTACAGTTC TTCAAGCAAG  | 1380 |
| CGCAGCAAAC GGCATGCGTG CGAGCATCTT TATTCAGCCT AAAGATGGTG GCCCTCTTCA  | 1440 |
| AACCTATGCA ATTCAATTCC TTGAAGAAGC GCCAAAATT GCTCACTTGA GCTTGCAAGT   | 1500 |
| GGAAAAAGCT GACAGTCTCA AAGAAGACCA AACTGTCAAA TTGTCGGTTC GAGCTACTA   | 1560 |
| TCAAGATGGA ACGCAAGCTG TATTACCAGC TGATAAAGTA ACCTTCTCTA CAAGTGGTGA  | 1620 |
| AGGGGAAGTC GCAATTCGTA AAGGAATGCT TGAGTTGCAT AAGCCAGGAG CAGTCACTCT  | 1680 |
| GAACGCTGAA TATGAGGGAG CTAAAGACCA AGTTGAACTC ACTATCCAAG CCAATACTGA  | 1740 |
| GAAGAAGATT GCGCAATCCA TCCGTCCTGT AAATGTAGTG ACAGATTTGC ATCAGGAACC  | 1800 |
| AAGTCTTCCA GCAACAGTAA CAGTTGAGTA TGACAAAGGT TTCCCTAAAA CTCATAAAGT  | 1860 |
| CACTTGGCAA GCTATTCCGA AAGAAAAACT AGACTCCTAT CAAACATTTG AAGTACTAGG  | 1920 |
| TAAAGTTGAA GGAATTGACC TTGAAGCGCG TGCAAAAAGTC TCTGTAGAAG GTATCGTTTC | 1980 |
| AGTTGAAGAA GTCAGTGTGA CAACTCCAAT CGCAGAAGCA CCACAATTAC CAGAAAGTGT  | 2040 |
| TCGGACATAT GATTCAAATG GTCACGTTTC ATCAGCTAAG GTTGCATGGG ATGCGATTTCG | 2100 |
| TCCAGAGCAA TACGCTAAGG AAGGTGTCTT TACAGTTAAT GGTCGCTTAG AAGGTACGCA  | 2160 |
| ATTAACA                                                            | 2167 |

## (2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 722 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His Asp Phe Tyr
1           5           10
Leu Tyr Gln Ser Gln Trp Val Ser Val Lys Lys Lys Pro Met Val His
20          25          30
Leu Leu Pro His Trp Asn Trp Glu Asn Lys Glu Leu Ala Ser Lys Val
35          40          45
Ala Asp Ser Glu Gly Lys Ile Pro Val Arg Ala Tyr Ser Asn Ala Ser
50          55          60
Ser Val Glu Leu Phe Leu Asn Gly Lys Ser Leu Gly Leu Lys Thr Phe
65          70          75          80
Asn Lys Lys Gln Thr Ser Asp Gly Arg Thr Tyr Gln Glu Gly Ala Asn
85          90          95
Ala Asn Glu Leu Tyr Leu Glu Trp Lys Val Ala Tyr Gln Pro Gly Thr
100         105         110
Leu Glu Ala Ile Ala Arg Asp Glu Ser Gly Lys Glu Ile Ala Arg Asp
115        120        125
Lys Ile Thr Thr Ala Gly Lys Pro Ala Ala Val Arg Leu Ile Lys Glu
130        135        140
Asp His Ala Ile Ala Ala Asp Gly Lys Asp Leu Thr Tyr Ile Tyr Tyr
145        150        155        160
Glu Ile Val Asp Ser Gln Gly Asn Val Val Pro Thr Ala Asn Asn Leu
165        170        175
Val Arg Phe Gln Leu His Gly Gln Gly Gln Leu Val Gly Val Asp Asn
180        185        190
Gly Glu Gln Ala Ser Arg Glu Arg Tyr Lys Ala Gln Ala Asp Gly Ser
195        200        205
Trp Ile Arg Lys Ala Phe Asn Gly Lys Gly Val Ala Ile Val Lys Ser
210        215        220
Thr Glu Gln Ala Gly Lys Phe Thr Leu Thr Ala His Ser Asp Leu Leu
225        230        235        240
Lys Ser Asn Gln Val Thr Val Phe Thr Gly Lys Lys Glu Gly Gln Glu
245        250        255
Lys Thr Val Leu Gly Thr Glu Val Pro Lys Val Gln Thr Ile Ile Gly
260        265        270
Glu Ala Pro Glu Met Pro Thr Thr Val Pro Phe Val Tyr Ser Asp Gly
275        280        285
Ser Arg Ala Glu Arg Pro Val Thr Trp Ser Ser Val Asp Val Ser Lys
290        295        300

```

Pro Gly Ile Val Thr Val Lys Gly Met Ala Asp Gly Arg Glu Val Glu  
 305 310 315 320  
 Ala Arg Val Glu Val Ile Ala Leu Lys Ser Glu Leu Pro Val Val Lys  
 325 330 335  
 Arg Ile Ala Pro Asn Thr Asp Leu Asn Ser Val Asp Lys Ser Val Ser  
 340 345 350  
 Tyr Val Leu Ile Asp Gly Ser Val Glu Glu Tyr Glu Val Asp Lys Trp  
 355 360 365  
 Glu Ile Ala Glu Glu Asp Lys Ala Lys Leu Ala Ile Pro Gly Ser Arg  
 370 375 380  
 Ile Gln Ala Thr Gly Tyr Leu Glu Gly Gln Pro Ile His Ala Thr Leu  
 385 390 395 400  
 Val Val Glu Glu Gly Asn Pro Ala Ala Pro Ala Val Pro Thr Val Thr  
 405 410 415  
 Val Gly Gly Glu Ala Val Thr Gly Leu Thr Ser Gln Lys Pro Met Gln  
 420 425 430  
 Tyr Arg Thr Leu Ala Tyr Gly Ala Lys Leu Pro Glu Val Thr Ala Ser  
 435 440 445  
 Ala Lys Asn Ala Ala Val Thr Val Leu Gln Ala Ser Ala Ala Asn Gly  
 450 455 460  
 Met Arg Ala Ser Ile Phe Ile Gln Pro Lys Asp Gly Gly Pro Leu Gln  
 465 470 475 480  
 Thr Tyr Ala Ile Gln Phe Leu Glu Glu Ala Pro Lys Ile Ala His Leu  
 485 490 495  
 Ser Leu Gln Val Glu Lys Ala Asp Ser Leu Lys Glu Asp Gln Thr Val  
 500 505 510  
 Lys Leu Ser Val Arg Ala His Tyr Gln Asp Gly Thr Gln Ala Val Leu  
 515 520 525  
 Pro Ala Asp Lys Val Thr Phe Ser Thr Ser Gly Glu Gly Glu Val Ala  
 530 535 540  
 Ile Arg Lys Gly Met Leu Glu Leu His Lys Pro Gly Ala Val Thr Leu  
 545 550 555 560  
 Asn Ala Glu Tyr Glu Gly Ala Lys Asp Gln Val Glu Leu Thr Ile Gln  
 565 570 575  
 Ala Asn Thr Glu Lys Lys Ile Ala Gln Ser Ile Arg Pro Val Asn Val  
 580 585 590  
 Val Thr Asp Leu His Gln Glu Pro Ser Leu Pro Ala Thr Val Thr Val  
 595 600 605  
 Glu Tyr Asp Lys Gly Phe Pro Lys Thr His Lys Val Thr Trp Gln Ala  
 610 615 620  
 Ile Pro Lys Glu Lys Leu Asp Ser Tyr Gln Thr Phe Glu Val Leu Gly  
 625 630 635 640  
 Lys Val Glu Gly Ile Asp Leu Glu Ala Arg Ala Lys Val Ser Val Glu

|                                                                 |                     |                     |             |  |     |
|-----------------------------------------------------------------|---------------------|---------------------|-------------|--|-----|
|                                                                 | 645                 |                     | 650         |  | 655 |
| Gly Ile Val                                                     | Ser Val Glu Glu Val | Ser Val Thr Thr Pro | Ile Ala Glu |  |     |
|                                                                 | 660                 | 665                 | 670         |  |     |
| Ala Pro Gln Leu Pro Glu Ser Val Arg Thr Tyr Asp Ser Asn Gly His |                     |                     |             |  |     |
|                                                                 | 675                 | 680                 | 685         |  |     |
| Val Ser Ser Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr |                     |                     |             |  |     |
|                                                                 | 690                 | 695                 | 700         |  |     |
| Ala Lys Glu Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln |                     |                     |             |  |     |
|                                                                 | 705                 | 710                 | 715         |  | 720 |
| Leu Thr                                                         |                     |                     |             |  |     |

## (2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2329 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| AGCTAAGGTT GCATGGGATG CGATTTCGTCC AGAGCAATAC GCTAAGGAAG GTGTCTTTAC | 60   |
| AGTTAATGGT CGCTTAGAAG GTACGCAATT AACAACTAAA CTTTCATGTTT GCGTATCTGC | 120  |
| TCAAACGTGAG CAAGGTGCAA ACATTTCTGA CCAATGGACC GGTTCAGAAT TGCCACTTGC | 180  |
| CTTTGCTTCA GACTCAAATC CAAGCGACCC AGTTTCAAAT GTTAATGACA AGCTCATTTT  | 240  |
| CTACAATAAC CAACCAGCCA ATCGTTGGAC AAACCTGGAAT CGTACTAATC CAGAAGCTTC | 300  |
| AGTCGGTGTT CTGTTTGGAG ATTCAGGTAT CTTGAGCAAA CGCTCCGTTG ATAATCTAAG  | 360  |
| TGTCGGATTC CATGAAGACC ATGGAGTTGG TGTACCGAAG TCTTATGTGA TTGAGTATTA  | 420  |
| TGTTGGTAAG ACTGTCCCAA CAGCTCCTAA AAACCCTAGT TTTGTTGGTA ATGAGGACCA  | 480  |
| TGTCTTTAAT GATTCTGCCA ACTGGAAACC AGTTACTAAT CTAAAAGCCC CTGCTCAACT  | 540  |
| CAAGGCTGGA GAAATGAACC ACTTTAGCTT TGATAAAGTT GAAACCTATG CTGTTTCGTAT | 600  |
| TCGCATGGTT AAAGCAGATA ACAAGCGTGG AACGTCTATC ACAGAGGTAC AAATCTTTGC  | 660  |
| GAAACAAGTT GCGGCAGCCA AGCAAGGACA AACAAGAATC CAAGTTGACG GCAAAGACTT  | 720  |
| AGCAAACCTC AACCTGATT TGACAGACTA CTACCTTGAG TCTGTAGATG GAAAAGTTCC   | 780  |
| GGCAGTCACA GCAAGTGTTA GCAACAATGG TCTCGCTACC GTCGTTCCAA GCGTTCGTGA  | 840  |
| AGGTGAGCCA GTTCGTGTCA TCGCGAAAGC TGAAAATGGC GACATCTTAG GAGAATACCG  | 900  |
| TCTGCACTTC ACTAAGGATA AGAGCTTACT TTCTCATAAA CCAGTTGCTG CGGTTAAACA  | 960  |
| AGCTCGCTTG CTACAAGTAG GTCAAGCACT TGAATTGCCG ACTAAGGTTT CAGTTTACTT  | 1020 |
| CACAGGTAAA GACGGCTACG AAACAAAAGA CCTGACAGTT GAATGGGAAG AAGTTCCAGC  | 1080 |

```

GGAAAATCTG ACAAAGCAG GTCAATTTAC TGTTCGAGGC CGTGTCTTGT GTAGTAACCT      1140
TGTTGCTGAG ATCACTGTAC GAGTGACAGA CAAACTTGGT GAGACTCTTT CAGATAACCC      1200
TAACTATGAT GAAAACAGTA ACCAGGCCTT TGCTTCAGCA ACCAATGATA TTGACAAAAA      1260
CTCTCATGAC CGCGTTGACT ATCTCAATGA CGGAGATCAT TCAGAAAATC GTCGTTGGAC      1320
AAACTGGTCA CCAACACCAT CTTCTAATCC AGAAGTATCA GCGGGTGTGA TTTTCCGTGA      1380
AAATGGTAAG ATTGTAGAAC GGACTGTTAC ACAAGGAAAA GTTCAGTTCT TTGCAGATAG      1440
TGGTACGGAT GCACCATCTA AACTCGTTTT AGAACGCTAT GTCGGTCCAG AGTTTGAAGT      1500
GCCAACCTAC TATTCAAACCT ACCAAGCCTA CGACGCAGAC CATCCATTCA ACAATCCAGA      1560
AAATTGGGAA GCTGTTCCCTT ATCGTGCGGA TAAAGACATT GCAGCTGGTG ATGAAATCAA      1620
CGTAACATTT AAAGCTATCA AAGCCAAAGC TATGAGATGG CGTATGGAGC GTAAAGCAGA      1680
TAAGAGCGGT GTTGCATGA TTGAGATGAC CTTCTTGCA CCAAGTGAAT TGCCTCAAGA      1740
AAGCACTCAA TCAAAGATTC TTGTAGATGG AAAAGAACTT GCTGATTTCT CTGAAAATCG      1800
TCAAGACTAT CAAATTACCT ATAAAGGTCA ACGGCCAAAA GTCTCAGTTG AAGAAAACAA      1860
TCAAGTAGCT TCAACTGTGG TAGATAGTGG AGAAGATAGC TTTCCAGTAC TTGTTGCTCT      1920
CGTTTCAGAA AGTGGAAAAC AAGTCAAGGA ATACCGTATC CACTTGACTA AGGAAAACC      1980
AGTTTCTGAG AAGACAGTTG CTGCTGTACA AGAAGATCTT CAAAAAATCG AATTTGTTGA      2040
AAAAGATTTG GCATACAAGA CAGTTGAGAA AAAAGATTCA AACTGTATC TAGGTGAAAC      2100
TCGTGTAGAA CAAGAAGGAA AAGTTGAAA AGAACGTATC TTTACAGCGA TTAATCCTGA      2160
TGGAAGTAAG GAAGAAAAAC TCCGTGAAGT GGTAGAAGTT CCGACAGACC GCATCGTCTT      2220
GGTTGGAACC AAACCAGTAG CTCAAGAAGC TAAAAACCA CAAGTGTGAG AAAAAGCAGA      2280
TACAAAACCA ATTGATTCAA GTGAAGCTAG TCAAATAAT AAAGCCCAG      2329

```

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```

Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr Ala Lys Glu
1      5      10
Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln Leu Thr Thr
      20      25      30
Lys Leu His Val Arg Val Ser Ala Gln Thr Glu Gln Gly Ala Asn Ile
      35      40      45

```

Ser Asp Gln Trp Thr Gly Ser Glu Leu Pro Leu Ala Phe Ala Ser Asp  
 50 55 60  
 Ser Asn Pro Ser Asp Pro Val Ser Asn Val Asn Asp Lys Leu Ile Ser  
 65 70 75 80  
 Tyr Asn Asn Gln Pro Ala Asn Arg Trp Thr Asn Trp Asn Arg Thr Asn  
 85 90 95  
 Pro Glu Ala Ser Val Gly Val Leu Phe Gly Asp Ser Gly Ile Leu Ser  
 100 105 110  
 Lys Arg Ser Val Asp Asn Leu Ser Val Gly Phe His Glu Asp His Gly  
 115 120 125  
 Val Gly Val Pro Lys Ser Tyr Val Ile Glu Tyr Tyr Val Gly Lys Thr  
 130 135 140  
 Val Pro Thr Ala Pro Lys Asn Pro Ser Phe Val Gly Asn Glu Asp His  
 145 150 155 160  
 Val Phe Asn Asp Ser Ala Asn Trp Lys Pro Val Thr Asn Leu Lys Ala  
 165 170 175  
 Pro Ala Gln Leu Lys Ala Gly Glu Met Asn His Phe Ser Phe Asp Lys  
 180 185 190  
 Val Glu Thr Tyr Ala Val Arg Ile Arg Met Val Lys Ala Asp Asn Lys  
 195 200 205  
 Arg Gly Thr Ser Ile Thr Glu Val Gln Ile Phe Ala Lys Gln Val Ala  
 210 215 220  
 Ala Ala Lys Gln Gly Gln Thr Arg Ile Gln Val Asp Gly Lys Asp Leu  
 225 230 235 240  
 Ala Asn Phe Asn Pro Asp Leu Thr Asp Tyr Tyr Leu Glu Ser Val Asp  
 245 250 255  
 Gly Lys Val Pro Ala Val Thr Ala Ser Val Ser Asn Asn Gly Leu Ala  
 260 265 270  
 Thr Val Val Pro Ser Val Arg Glu Gly Glu Pro Val Arg Val Ile Ala  
 275 280 285  
 Lys Ala Glu Asn Gly Asp Ile Leu Gly Glu Tyr Arg Leu His Phe Thr  
 290 295 300  
 Lys Asp Lys Ser Leu Leu Ser His Lys Pro Val Ala Ala Val Lys Gln  
 305 310 315 320  
 Ala Arg Leu Leu Gln Val Gly Gln Ala Leu Glu Leu Pro Thr Lys Val  
 325 330 335  
 Pro Val Tyr Phe Thr Gly Lys Asp Gly Tyr Glu Thr Lys Asp Leu Thr  
 340 345 350  
 Val Glu Trp Glu Glu Val Pro Ala Glu Asn Leu Thr Lys Ala Gly Gln  
 355 360 365  
 Phe Thr Val Arg Gly Arg Val Leu Gly Ser Asn Leu Val Ala Glu Ile  
 370 375 380

Thr Val Arg Val Thr Asp Lys Leu Gly Glu Thr Leu Ser Asp Asn Pro  
 385 390 395 400  
 Asn Tyr Asp Glu Asn Ser Asn Gln Ala Phe Ala Ser Ala Thr Asn Asp  
 405 410 415  
 Ile Asp Lys Asn Ser His Asp Arg Val Asp Tyr Leu Asn Asp Gly Asp  
 420 425 430  
 His Ser Glu Asn Arg Arg Trp Thr Asn Trp Ser Pro Thr Pro Ser Ser  
 435 440 445  
 Asn Pro Glu Val Ser Ala Gly Val Ile Phe Arg Glu Asn Gly Lys Ile  
 450 455 460  
 Val Glu Arg Thr Val Thr Gln Gly Lys Val Gln Phe Phe Ala Asp Ser  
 465 470 475 480  
 Gly Thr Asp Ala Pro Ser Lys Leu Val Leu Glu Arg Tyr Val Gly Pro  
 485 490 495  
 Glu Phe Glu Val Pro Thr Tyr Tyr Ser Asn Tyr Gln Ala Tyr Asp Ala  
 500 505 510  
 Asp His Pro Phe Asn Asn Pro Glu Asn Trp Glu Ala Val Pro Tyr Arg  
 515 520 525  
 Ala Asp Lys Asp Ile Ala Ala Gly Asp Glu Ile Asn Val Thr Phe Lys  
 530 535 540  
 Ala Ile Lys Ala Lys Ala Met Arg Trp Arg Met Glu Arg Lys Ala Asp  
 545 550 555 560  
 Lys Ser Gly Val Ala Met Ile Glu Met Thr Phe Leu Ala Pro Ser Glu  
 565 570 575  
 Leu Pro Gln Glu Ser Thr Gln Ser Lys Ile Leu Val Asp Gly Lys Glu  
 580 585 590  
 Leu Ala Asp Phe Ala Glu Asn Arg Gln Asp Tyr Gln Ile Thr Tyr Lys  
 595 600 605  
 Gly Gln Arg Pro Lys Val Ser Val Glu Glu Asn Asn Gln Val Ala Ser  
 610 615 620  
 Thr Val Val Asp Ser Gly Glu Asp Ser Phe Pro Val Leu Val Arg Leu  
 625 630 635 640  
 Val Ser Glu Ser Gly Lys Gln Val Lys Glu Tyr Arg Ile His Leu Thr  
 645 650 655  
 Lys Glu Lys Pro Val Ser Glu Lys Thr Val Ala Ala Val Gln Glu Asp  
 660 665 670  
 Leu Pro Lys Ile Glu Phe Val Glu Lys Asp Leu Ala Tyr Lys Thr Val  
 675 680 685  
 Glu Lys Lys Asp Ser Thr Leu Tyr Leu Gly Glu Thr Arg Val Glu Gln  
 690 695 700  
 Glu Gly Lys Val Gly Lys Glu Arg Ile Phe Thr Ala Ile Asn Pro Asp  
 705 710 715 720  
 Gly Ser Lys Glu Glu Lys Leu Arg Glu Val Val Glu Val Pro Thr Asp

[illegible]

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CTATCACTAT GTAAATAAAG AGATTATTTT ACAAGAAGCT AAAGATTTTAA TTCAGACAGG | 60  |
| AAAGCCTGAC AGGAATGAAG TTGTATATGG TTTGGTGTAT CAAAAAGATC AGTTGCCTCA  | 120 |
| AACAGGGACA GAA                                                     | 133 |

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 44 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Tyr His Tyr Val Asn Lys Glu Ile Ile Ser Gln Glu Ala Lys Asp Leu  
1 5 10 15  
Ile Gln Thr Gly Lys Pro Asp Arg Asn Glu Val Val Tyr Gly Leu Val  
20 25 30  
Tyr Gln Lys Asp Gln Leu Pro Gln Thr Gly Thr Glu  
35 40

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TGAGACTCCT CAATCAATAA CAAATCAGGA GCAAGCTAGG ACAGAAAACC AAGTAGTAGA 60

```

GACAGAGGAA GCTCCAAAAG AAGAAGCACC TAAAACAGAA GAAAGTCCAA AGGAAGAACC      120
AAAATCGGAG GTAAAACCTA CTGACGACAC CCTTCCTAAA GTAGAAGAGG GGAAAGAAGA      180
TTCAGCAGAA CCAGCTCCAG TTGAAGAAGT AGGTGGAGAA GTTGAGTCAA AACCAGAGGA      240
AAAAGTAGCA GTTAAGCCAG AAAGTCAACC ATCAGACAAA CCAGCTGAGG AATCAAAAAGT      300
TGAACAAGCA GGTGAACCAG TCGCGCCAAG AGAAGACGAA AAGGCACCAG TCGAGCCAGA      360
AAAGCAACCA GAAGCTCCTG AAGAAGAGAA GGCTGTAGAG GAAACACCGA AACAAGAAGA      420
GTCAACTCCA GATACCAAGG CTGAAGAAAC TGTAGAACCA AAAGAGGAGA CTGTTAATCA      480
ATCTATTGAA CAACCAAAAAG TTGAAACGCC TGCTGTAGAA AAACAAACAG AACCAACAGA      540
GGAACCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AACAGGCACC      600
AACGGCACCA GTTGAGCCAG AAAAGCAACC AGAAGTTCCT GAAGAAGAGA AGGCTGTAGA      660
GGAAACACCG AAACCAGAAG ATAAAATAAA GGGTATTGGT ACTAAAGAAC CAGTTGATAA      720
AAGTGAGTTA AATAATCAAA TTGATAAAGC TAGTTCAGTT TCTCCTACTG ATTAT          775

```

## (2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 258 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```

Glu Thr Pro Gln Ser Ile Thr Asn Gln Glu Gln Ala Arg Thr Glu Asn
1          5          10          15
Gln Val Val Glu Thr Glu Glu Ala Pro Lys Glu Glu Ala Pro Lys Thr
20          25          30
Glu Glu Ser Pro Lys Glu Glu Pro Lys Ser Glu Val Lys Pro Thr Asp
35          40          45
Asp Thr Leu Pro Lys Val Glu Glu Gly Lys Glu Asp Ser Ala Glu Pro
50          55          60
Ala Pro Val Glu Glu Val Gly Gly Glu Val Glu Ser Lys Pro Glu Glu
65          70          75          80
Lys Val Ala Val Lys Pro Glu Ser Gln Pro Ser Asp Lys Pro Ala Glu
85          90          95
Glu Ser Lys Val Glu Gln Ala Gly Glu Pro Val Ala Pro Arg Glu Asp
100         105         110
Glu Lys Ala Pro Val Glu Pro Glu Lys Gln Pro Glu Ala Pro Glu Glu
115         120         125
Glu Lys Ala Val Glu Glu Thr Pro Lys Gln Glu Glu Ser Thr Pro Asp
130         135         140

```

Thr Lys Ala Glu Glu Thr Val Glu Pro Lys Glu Glu Thr Val Asn Gln  
 145 150 155 160  
 Ser Ile Glu Gln Pro Lys Val Glu Thr Pro Ala Val Glu Lys Gln Thr  
 165 170 175  
 Glu Pro Thr Glu Glu Pro Lys Val Glu Gln Ala Gly Glu Pro Val Ala  
 180 185 190  
 Pro Arg Glu Asp Glu Gln Ala Pro Thr Ala Pro Val Glu Pro Glu Lys  
 195 200 205  
 Gln Pro Glu Val Pro Glu Glu Glu Lys Ala Val Glu Glu Thr Pro Lys  
 210 215 220  
 Pro Glu Asp Lys Ile Lys Gly Ile Gly Thr Lys Glu Pro Val Asp Lys  
 225 230 235 240  
 Ser Glu Leu Asn Asn Gln Ile Asp Lys Ala Ser Ser Val Ser Pro Thr  
 245 250 255  
 Asp Tyr

## (2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 199 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

GGATGCTCAA GAAACTGCGG GAGTTCAC TAATATGTG GCAGATTCAG AGCTATCATC 60  
 AGAAGAAAAG AAGCAGCTTG TCTATGATAT TCCGACATAC GTGGAGAATG ATGATGAAAC 120  
 TTATTATCTT GTTATAAGT TAAATTCTCA AAATCAACTG GCGGAATTGC CAAATACTGG 180  
 AAGCAAGAAT GAGAGGCAA 199

## (2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Asp Ala Gln Glu Thr Ala Gly Val His Tyr Lys Tyr Val Ala Asp Ser  
 1 5 10 15  
 Glu Leu Ser Ser Glu Glu Lys Lys Gln Leu Val Tyr Asp Ile Pro Thr  
 20 25 30

Tyr Val Glu Asn Asp Asp Glu Thr Tyr Tyr Leu Val Tyr Lys Leu Asn  
 35 40 45  
 Ser Gln Asn Gln Leu Ala Glu Leu Pro Asn Thr Gly Ser Lys Asn Glu  
 50 55 60  
 Arg Gln  
 65

## (2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 835 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CGACAAAGGT GAGACTGAGG TTCAACCAGA GTCGCCAGAT ACTGTGGTAA GTGATAAAGG 60  
 TGAACCAGAG CAGGTAGCAC CGCTTCCAGA ATATAAGGGT AATATTGAGC AAGTAAAACC 120  
 TGAAACTCCG GTTGAGAAGA CCAAAGAACA AGGTCCAGAA AAAACTGAAG AAGTTCCAGT 180  
 AAAACCAACA GAAGAAACAC CAGTAAATCC AAATGAAGGT ACTACAGAAG GAACCTCAAT 240  
 TCAAGAAGCA GAAAATCCAG TTCAACCTGC AGAAGAATCA ACAACGAATT CAGAGAAAGT 300  
 ATCACCAGAT ACATCTAGCA AAAATACTGG GGAAGTGTCC AGTAATCCTA GTGATTTCGAC 360  
 AACCTCAGTT GGAGAATCAA ATAAACCAGA ACATAATGAC TCTAAAAATG AAAATTCAGA 420  
 AAAAAGTGT GAAGAAGTTC CAGTAAATCC AAATGAAGGC ACAGTAGAAG GTACCTCAAA 480  
 TCAAGAAACA GAAAAACCAG TTCAACCTGC AGAAGAAACA CAAACAAACT CTGGGAAAAT 540  
 AGCTAACGAA AATACTGGAG AAGTATCCAA TAAACCTAGT GATTCAAAAC CACCAGTTGA 600  
 AGAATCAAAT CAACCAGAAA AAAACGGAAC TGCAACAAAA CCAGAAAATT CAGGTAATAC 660  
 AACATCAGAG AATGGACAAA CAGAACCAGA ACCATCAAAC GGAAATTCAA CTGAGGATGT 720  
 TTCAACCGAA TCAAACACAT CCAATTCAA TGGAAACGAA GAAATTAAAC AAGAAAATGA 780  
 ACTAGACCCT GATAAAAAGG TAGAAGAACC AGAGAAAACA CTTGAATTAA GAAAT 835

## (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 278 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp Lys Gly Glu Thr Glu Val Gln Pro Glu Ser Pro Asp Thr Val Val  
 1 5 10 15

Ser Asp Lys Gly Glu Pro Glu Gln Val Ala Pro Leu Pro Glu Tyr Lys  
                   20                                  25                                  30  
 Gly Asn Ile Glu Gln Val Lys Pro Glu Thr Pro Val Glu Lys Thr Lys  
                   35                                  40                                  45  
 Glu Gln Gly Pro Glu Lys Thr Glu Glu Val Pro Val Lys Pro Thr Glu  
                   50                                  55                                  60  
 Glu Thr Pro Val Asn Pro Asn Glu Gly Thr Thr Glu Gly Thr Ser Ile  
                   65                                  70                                  75                                  80  
 Gln Glu Ala Glu Asn Pro Val Gln Pro Ala Glu Glu Ser Thr Thr Asn  
                                   85                                  90                                  95  
 Ser Glu Lys Val Ser Pro Asp Thr Ser Ser Lys Asn Thr Gly Glu Val  
                                   100                                  105                                  110  
 Ser Ser Asn Pro Ser Asp Ser Thr Thr Ser Val Gly Glu Ser Asn Lys  
                                   115                                  120                                  125  
 Pro Glu His Asn Asp Ser Lys Asn Glu Asn Ser Glu Lys Thr Val Glu  
                                   130                                  135                                  140  
 Glu Val Pro Val Asn Pro Asn Glu Gly Thr Val Glu Gly Thr Ser Asn  
                                   145                                  150                                  155                                  160  
 Gln Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn  
                                   165                                  170                                  175  
 Ser Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro  
                                   180                                  185                                  190  
 Ser Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn  
                                   195                                  200                                  205  
 Gly Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn  
                                   210                                  215                                  220  
 Gly Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val  
                                   225                                  230                                  235                                  240  
 Ser Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys  
                                   245                                  250                                  255  
 Gln Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys  
                                   260                                  265                                  270  
 Thr Leu Glu Leu Arg Asn  
                                   275

## (2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 709 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```

AAATCAATTG GTAGCACAAG ATCCAAAAGC ACAAGATAGC ACTAAACTGA CTGCTGAAAA      60
ATCAACTGTT AAAGCACCTG CTCAAAGAGT AGATGTAAAA GATATAACTC ATTTAACAGA      120
TGAAGAAAAA GTTAAGGTTG CTATTTTACA AGCAAATGGT TCAGCATTAG ACGGAGCGAC      180
AATCAATGTA GCTGGAGATG GTACAGCAAC AATCACATTC CCAGATGGTT CAGTAGTGAC      240
GATTCTAGGA AAAGATACAG TTCAACAATC TGCGAAAGGT GAATCTGTAA CTCAAGAAGC      300
TACACCAGAG TATAAGCTAG AAAATACACC AGGTGGAGAT AAGGGAGGCA ATACTGGAAG      360
CTCAGATGCT AATGCGAATG AAGGCGGTGG TAGCCAGGCG GGTGGATCAG CTCACACAGG      420
TTCACAAAAC TCAGCTCAAT CACAAGCTTC TAAGCAATTA GCTACTGAAA AAGAATCAGC      480
TAAAAATGCC ATTGAAAAAG CAGCCAAGGA CAAGCAGGAT GAAATCAAAG GCGCACCCTG      540
TTCTGATAAA GAAAAAGCAG AACTTTTTCAGC AAGAGTGGAA GCAGAAAAAC AAGCAGCTCT      600
CAAAGAGATT GAAAATGCGA AACTATGGA AGATGTGAAG GAAGCAGAAA CGATTGGAGT      660
GCAAGCCATT GCCATGGTTA CAGTTCCTAA GAGACCAAGT GCTCCTAAT      709

```

## (2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 236 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```

Asn Gln Leu Val Ala Gln Asp Pro Lys Ala Gln Asp Ser Thr Lys Leu
1           5           10           15
Thr Ala Glu Lys Ser Thr Val Lys Ala Pro Ala Gln Arg Val Asp Val
20          25          30
Lys Asp Ile Thr His Leu Thr Asp Glu Glu Lys Val Lys Val Ala Ile
35          40          45
Leu Gln Ala Asn Gly Ser Ala Leu Asp Gly Ala Thr Ile Asn Val Ala
50          55          60
Gly Asp Gly Thr Ala Thr Ile Thr Phe Pro Asp Gly Ser Val Val Thr
65          70          75          80
Ile Leu Gly Lys Asp Thr Val Gln Gln Ser Ala Lys Gly Glu Ser Val
85          90          95
Thr Gln Glu Ala Thr Pro Glu Tyr Lys Leu Glu Asn Thr Pro Gly Gly
100         105         110
Asp Lys Gly Gly Asn Thr Gly Ser Ser Asp Ala Asn Ala Asn Glu Gly
115         120         125
Gly Gly Ser Gln Ala Gly Gly Ser Ala His Thr Gly Ser Gln Asn Ser
130         135         140

```

Ala Gln Ser Gln Ala Ser Lys Gln Leu Ala Thr Glu Lys Glu Ser Ala  
 145 150 155 160  
 Lys Asn Ala Ile Glu Lys Ala Ala Lys Asp Lys Gln Asp Glu Ile Lys  
 165 170 175  
 Gly Ala Pro Leu Ser Asp Lys Glu Lys Ala Glu Leu Leu Ala Arg Val  
 180 185 190  
 Glu Ala Glu Lys Gln Ala Ala Leu Lys Glu Ile Glu Asn Ala Lys Thr  
 195 200 205  
 Met Glu Asp Val Lys Glu Ala Glu Thr Ile Gly Val Gln Ala Ile Ala  
 210 215 220  
 Met Val Thr Val Pro Lys Arg Pro Val Ala Pro Asn  
 225 230 235

## (2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 787 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CAAACAGTCA GCTTCAGGAA CGATTGAGGT GATTTACGA GAAAATGGCT CTGGGACACG 60  
 GGGTGCCTTC ACAGAAATCA CAGGGATTCT CAAAAAGAC GGTGATAAAA AAATTGACAA 120  
 CACTGCCAAA ACAGCTGTGA TTCAAATAG TACAGAAGGT GTTCTCTCAG CAGTTCAAGG 180  
 GAATGCTAAT GCTATCGGCT ACATCTCCTT GGGATCTTTA ACGAAATCTG TCAAGGCTTT 240  
 AGAGATTGAT GGTGTCAAGG CTAGTCGAGA CACAGTTTTA GATGGTGAAT ACCCTCTTCA 300  
 ACGTCCCTTC AACATTGTTT GGTCTTCTAA TCTTTCCAAG CTAGGTCAAG ATTTTATCAG 360  
 CTTTATCCAC TCCAAACAAG GTCAACAAGT GGTCACAGAT AATAAATTTA TTGAAGCTAA 420  
 AACCGAAACC ACGGAATATA CAAGCCAACA CTTATCAGGC AAGTTGTCTG TTGTAGGTTC 480  
 CACTTCAGTA TCTTCTTTAA TGGAAAAATT AGCAGAAGCT TATAAAAAAG AAAATCCAGA 540  
 AGTTACGATT GATATTACCT CTAATGGGTC TTCAGCAGGT ATTACCGCTG TTAAGGAGAA 600  
 AACCGCTGAT ATTGGTATGG TTTCTAGGGA ATTAACCTCCT GAAGAAGGTA AGAGTCTCAC 660  
 CCATGATGCT ATTGCTTTAG ACGGTATTGC TGTGTGGTC AATAATGACA ATAAGGCAAG 720  
 CCAAGTCAGT ATGGCTGAAC TTGCAGACGT TTTTAGTGGC AAATTAACCA CCTGGGACAA 780  
 GATTAAA 787

## (2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 262 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gln | Ser | Ala | Ser | Gly | Thr | Ile | Glu | Val | Ile | Ser | Arg | Glu | Asn | Gly | 1   | 5   | 10  | 15  |
| Ser | Gly | Thr | Arg | Gly | Ala | Phe | Thr | Glu | Ile | Thr | Gly | Ile | Leu | Lys | Lys | 20  | 25  | 30  |     |
| Asp | Gly | Asp | Lys | Lys | Ile | Asp | Asn | Thr | Ala | Lys | Thr | Ala | Val | Ile | Gln | 35  | 40  | 45  |     |
| Asn | Ser | Thr | Glu | Gly | Val | Leu | Ser | Ala | Val | Gln | Gly | Asn | Ala | Asn | Ala | 50  | 55  | 60  |     |
| Ile | Gly | Tyr | Ile | Ser | Leu | Gly | Ser | Leu | Thr | Lys | Ser | Val | Lys | Ala | Leu | 65  | 70  | 75  | 80  |
| Glu | Ile | Asp | Gly | Val | Lys | Ala | Ser | Arg | Asp | Thr | Val | Leu | Asp | Gly | Glu | 85  | 90  | 95  |     |
| Tyr | Pro | Leu | Gln | Arg | Pro | Phe | Asn | Ile | Val | Trp | Ser | Ser | Asn | Leu | Ser | 100 | 105 | 110 |     |
| Lys | Leu | Gly | Gln | Asp | Phe | Ile | Ser | Phe | Ile | His | Ser | Lys | Gln | Gly | Gln | 115 | 120 | 125 |     |
| Gln | Val | Val | Thr | Asp | Asn | Lys | Phe | Ile | Glu | Ala | Lys | Thr | Glu | Thr | Thr | 130 | 135 | 140 |     |
| Glu | Tyr | Thr | Ser | Gln | His | Leu | Ser | Gly | Lys | Leu | Ser | Val | Val | Gly | Ser | 145 | 150 | 155 | 160 |
| Thr | Ser | Val | Ser | Ser | Leu | Met | Glu | Lys | Leu | Ala | Glu | Ala | Tyr | Lys | Lys | 165 | 170 | 175 |     |
| Glu | Asn | Pro | Glu | Val | Thr | Ile | Asp | Ile | Thr | Ser | Asn | Gly | Ser | Ser | Ala | 180 | 185 | 190 |     |
| Gly | Ile | Thr | Ala | Val | Lys | Glu | Lys | Thr | Ala | Asp | Ile | Gly | Met | Val | Ser | 195 | 200 | 205 |     |
| Arg | Glu | Leu | Thr | Pro | Glu | Glu | Gly | Lys | Ser | Leu | Thr | His | Asp | Ala | Ile | 210 | 215 | 220 |     |
| Ala | Leu | Asp | Gly | Ile | Ala | Val | Val | Val | Asn | Asn | Asp | Asn | Lys | Ala | Ser | 225 | 230 | 235 | 240 |
| Gln | Val | Ser | Met | Ala | Glu | Leu | Ala | Asp | Val | Phe | Ser | Gly | Lys | Leu | Thr | 245 | 250 | 255 |     |
| Thr | Trp | Asp | Lys | Ile | Lys | 260 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 421 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

ATTTCGATGAT GCGGATGAAA AGATGACCCG TGATGAAATT GCCTATATGC TGACAAATAG      60
TGAAGAAACA TTGGATGCTG ATGAGATTGA GATGCTACAA GGTGTCTTTT CGCTCGATGA      120
ACTGATGGCA CGAGAGGTTA TGGTTCCTCG AACGGATGCC TTTATGGTGG ATATTCAGGA      180
TGATAGTCAA GCCATTATCC AAAGTATTTT AAAACAAAAT TATTCTCGTA TCCCGGTTTA      240
TGATGGGGAT AAGGACAATG TAATTGGAAT CATTACACACC AAGAGTCTCC TTAAGGCAGG      300
CTTTGTGGAC GGTTTTGACA ATATTGTTTG GAAGAGAATT TTACAAGATC CACTTTTTGT      360
ACCTGAAACT ATTTTGTGG ATGACTTGCT AAAAGAACTG CGAAATACCC AAAGACAAAT      420
G   421

```

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

Phe Asp Asp Ala Asp Glu Lys Met Thr Arg Asp Glu Ile Ala Tyr Met
1          5          10          15
Leu Thr Asn Ser Glu Glu Thr Leu Asp Ala Asp Glu Ile Glu Met Leu
20        25        30
Gln Gly Val Phe Ser Leu Asp Glu Leu Met Ala Arg Glu Val Met Val
35        40        45
Pro Arg Thr Asp Ala Phe Met Val Asp Ile Gln Asp Asp Ser Gln Ala
50        55        60
Ile Ile Gln Ser Ile Leu Lys Gln Asn Tyr Ser Arg Ile Pro Val Tyr
65        70        75
Asp Gly Asp Lys Asp Asn Val Ile Gly Ile Ile His Thr Lys Ser Leu
85        90        95
Leu Lys Ala Gly Phe Val Asp Gly Phe Asp Asn Ile Val Trp Lys Arg
100       105       110
Ile Leu Gln Asp Pro Leu Phe Val Pro Glu Thr Ile Phe Val Asp Asp
115       120       125
Leu Leu Lys Glu Leu Arg Asn Thr Gln Arg Gln Met
130       135       140

```

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

GGAGAGTCGA TCAAAAGTAG ATGAAGCTGT GTCTAAGTTT GAAAAGGACT CATCTTCTTC      60
GTCAAGTTCA GACTCTTCCA CTAAACCGGA AGCTTCAGAT ACAGCGAAGC CAAACAAGCC      120
GACAGAACCA GGAGAAAAGG TAGCAGAAGC TAAGAAGAAG GTTGAAGAAG CTGAGAAAAA      180
AGCCAAGGAT CAAAAGAAG AAGATCGTCG TAACTACCCA ACCATTACTT ACAAACGCT      240
TGAAGTTGAA ATTGCTGAGT CCGATGTGGA AGTTAAAAAA GCGGAGCTTG AACTAGTAAA      300
AGTGAAAGCT AACGAACCTC GAGACGAGCA A                                331
  
```

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 110 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

Glu Ser Arg Ser Lys Val Asp Glu Ala Val Ser Lys Phe Glu Lys Asp
1          5          10          15
Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Lys Pro Glu Ala Ser
20        25        30
Asp Thr Ala Lys Pro Asn Lys Pro Thr Glu Pro Gly Glu Lys Val Ala
35        40        45
Glu Ala Lys Lys Lys Val Glu Glu Ala Glu Lys Lys Ala Lys Asp Gln
50        55        60
Lys Glu Glu Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys Thr Leu
65        70        75        80
Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala Glu Leu
85        90        95
Glu Leu Val Lys Val Lys Ala Asn Glu Pro Arg Asp Glu Gln
100       105       110
  
```

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATGGACAACA GGAAACTGGG ACGAGGTTAT ATCTGGTAAG ATTGACAAGT ACAAAGATCC | 60  |
| AGATATTCCA ACAGTTGAAT CACAAGAAGT TACGTCAGAC TCTAGTGATA AAGAAATAAC | 120 |
| GGTAAGGTAT GACCGTTTAT CAACACCAGA AAAACCAATC CCACAACCAA ATCCAGAGCA | 180 |
| TCCAAGTGTT CCGACACCAA ACCCAGAACT ACCAAATCAA GAGACTCCAA CACCAGATAA | 240 |
| ACCAACTCCA GAACCAGGTA CTCCAAAAAC TGAAACTCCA GTGAATCCAG ACCCAGAAGT | 300 |
| TCCGACTTAT GAGACAGGTA AGAGAGAGGA ATTGCCAAAC ACAGGTACAG AAGCTAAT   | 358 |

## (2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 119 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Trp | Thr | Thr | Gly | Asn | Trp | Asp | Glu | Val | Ile | Ser | Gly | Lys | Ile | Asp | Lys | 1   | 5   | 10  | 15 |
| Tyr | Lys | Asp | Pro | Asp | Ile | Pro | Thr | Val | Glu | Ser | Gln | Glu | Val | Thr | Ser | 20  | 25  | 30  |    |
| Asp | Ser | Ser | Asp | Lys | Glu | Ile | Thr | Val | Arg | Tyr | Asp | Arg | Leu | Ser | Thr | 35  | 40  | 45  |    |
| Pro | Glu | Lys | Pro | Ile | Pro | Gln | Pro | Asn | Pro | Glu | His | Pro | Ser | Val | Pro | 50  | 55  | 60  |    |
| Thr | Pro | Asn | Pro | Glu | Leu | Pro | Asn | Gln | Glu | Thr | Pro | Thr | Pro | Asp | Lys | 65  | 70  | 75  | 80 |
| Pro | Thr | Pro | Glu | Pro | Gly | Thr | Pro | Lys | Thr | Glu | Thr | Pro | Val | Asn | Pro | 85  | 90  | 95  |    |
| Asp | Pro | Glu | Val | Pro | Thr | Tyr | Glu | Thr | Gly | Lys | Arg | Glu | Glu | Leu | Pro | 100 | 105 | 110 |    |
| Asn | Thr | Gly | Thr | Glu | Ala | Asn |     |     |     |     |     |     |     |     |     | 115 |     |     |    |

## (2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1879 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| CGATGGGCTC AATCCAACCC CAGGTCAAGT CTTACCTGAA GAGACATCGG GAACGAAAGA | 60   |
| GGGTGACTTA TCAGAAAAAC CAGGAGACAC CGTTCTCACT CAAGCGAAAC CTGAGGGCGT | 120  |
| TACTGGAAAT ACGAATTCAC TTCCGACACC TACAGAAAGA ACTGAAGTGA GCGAGGAAAC | 180  |
| AAGCCCTTCT AGTCTGGATA CACTTTTTGA AAAAGATGAA GAAGCTCAAA AAAATCCAGA | 240  |
| GCTAACAGAT GTCTTAAAG AAAGTGTAGA TACAGCTGAT GTGGATGGGA CACAAGCAAG  | 300  |
| TCCAGCAGAA ACTACTCCTG AACAAGTAAA AGGTGGAGTG AAAGAAAATA CAAAAGACAG | 360  |
| CATCGATGTT CCTGCTGCTT ATCTTGAAAA AGCTGAAGGG AAAGGTCCTT TCACTGCCGG | 420  |
| TGTAAACCAA GTAATTCCTT ATGAACTATT CGCTGGTGAT GGTATGTAA CTCGTCTATT  | 480  |
| ACTAAAAGCT TCGGATAATG CTCCTTGGTC TGACAATGGT ACTGCTAAAA ATCCTGCTTT | 540  |
| ACCTCCTCTT GAAGGATTAA CAAAAGGGAA ATACTTCTAT GAAGTAGACT TAAATGGCAA | 600  |
| TACTGTTGGT AAACAAGGTC AAGCTTTAAT TGATCAACTT CGCGCTAATG GTACTCAAAC | 660  |
| TTATAAGCT ACTGTTAAAG TTTACGAAA TAAAGACGGT AAAGCTGACT TGAATAATCT   | 720  |
| AGTTGCTACT AAAAATGTAG ACATCAACAT CAATGGATTA GTTGCTAAAG AAACAGTTCA | 780  |
| AAAAGCCGTT GCAGACAACG TTAAAGACAG TATCGATGTT CCAGCAGCCT ACCTAGAAAA | 840  |
| AGCCAAGGGT GAAGGTCCAT TCACAGCAGG TGTCAACCAT GTGATTCCAT ACGAACTCTT | 900  |
| CGCAGGTGAT GGCATGTTGA CTCGTCTCTT GCTCAAGGCA TCTGACAAGG CACCATGGTC | 960  |
| AGATAACGGC GACGCTAAAA ACCCAGCCCT ATCTCCACTA GGCGAAAACG TGAAGACCAA | 1020 |
| AGGTCAATAC TTCTATCAAN TAGCCTTGA CGGAAATGTA GCTGGCAAAG AAAAACAAGC  | 1080 |
| GCTCATTGAC CAGTTCCGAG CAAANGGTAC TCAAACTTAC AGCGCTACAG TCAATGTCTA | 1140 |
| TGGTAACAAA GACGGTAAAC CAGACTTGA CAACATCGTA GCAACTAAAA AAGTCACTAT  | 1200 |
| TAACATAAAC GGTTTAATTT CTAAAGAAAC AGTTCAAAAA GCCGTTGCAG ACAACGTAA  | 1260 |
| NGACAGTATC GATGTTCCAG CAGCCTACCT AGAAAAAGCC AAGGGTGAAG GTCCATTAC  | 1320 |
| AGCAGGTGTC AACCATGTGA TTCCATACGA ACTCTTCGCA GGTGATGGTA TGTTGACTCG | 1380 |
| TCTCTTGCTC AAGGCATCTG ACAAGGCACC ATGGTCAGAT AACGGNGACG CTAAAAACCC | 1440 |
| AGCNCTATCT CCACTAGGTG AAAACGTGAA GACCAAAGGT CAATACTTCT ATCAANTAGC | 1500 |
| CTTGACGGA AATGTAGCTG GCAAAGAAAA ACAAGCGCTC ATTGACCAGT TCCGAGCAAA  | 1560 |
| CGGTACTCAA ACTTACAGCG CTACAGTCAA TGTCTATGGT AACAAAGACG GTAAACCAGA | 1620 |
| CTTGACAAC ATCGTAGCAA CTAAAAAGT CACTATTAAG ATAAATGTTA AAGAAACATC   | 1680 |
| AGACACAGCA AATGGTTCAT TATCACCTTC TAACTCTGGT TCTGGCGTGA CTCCGATGAA | 1740 |
| TCACAATCAT GCTACAGGTA CTACAGATAG CATGCCTGCT GACACCATGA CAAGTTCTAC | 1800 |
| CAACACGATG GCAGGTGAAA ACATGGCTGC TTCTGCTAAC AAGATGTCTG ATACGATGAT | 1860 |
| GTCAGAGGAT AAAGCTATG                                              | 1879 |

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

Asp Gly Leu Asn Pro Thr Pro Gly Gln Val Leu Pro Glu Glu Thr Ser
1          5          10          15
Gly Thr Lys Glu Gly Asp Leu Ser Glu Lys Pro Gly Asp Thr Val Leu
20          25          30
Thr Gln Ala Lys Pro Glu Gly Val Thr Gly Asn Thr Asn Ser Leu Pro
35          40          45
Thr Pro Thr Glu Arg Thr Glu Val Ser Glu Glu Thr Ser Pro Ser Ser
50          55          60
Leu Asp Thr Leu Phe Glu Lys Asp Glu Glu Ala Gln Lys Asn Pro Glu
65          70          75          80
Leu Thr Asp Val Leu Lys Glu Thr Val Asp Thr Ala Asp Val Asp Gly
85          90          95
Thr Gln Ala Ser Pro Ala Glu Thr Thr Pro Glu Gln Val Lys Gly Gly
100         105         110
Val Lys Glu Asn Thr Lys Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu
115         120         125
Glu Lys Ala Glu Gly Lys Gly Pro Phe Thr Ala Gly Val Asn Gln Val
130         135         140
Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu
145         150         155         160
Leu Lys Ala Ser Asp Asn Ala Pro Trp Ser Asp Asn Gly Thr Ala Lys
165         170         175
Asn Pro Ala Leu Pro Pro Leu Glu Gly Leu Thr Lys Gly Lys Tyr Phe
180         185         190
Tyr Glu Val Asp Leu Asn Gly Asn Thr Val Gly Lys Gln Gly Gln Ala
195         200         205
Leu Ile Asp Gln Leu Arg Ala Asn Gly Thr Gln Thr Tyr Lys Ala Thr
210         215         220
Val Lys Val Tyr Gly Asn Lys Asp Gly Lys Ala Asp Leu Thr Asn Leu
225         230         235         240
Val Ala Thr Lys Asn Val Asp Ile Asn Ile Asn Gly Leu Val Ala Lys
245         250         255
Glu Thr Val Gln Lys Ala Val Ala Asp Asn Val Lys Asp Ser Ile Asp
260         265         270

```

Val Pro Ala Ala Tyr Leu Glu Lys Ala Lys Gly Glu Gly Pro Phe Thr  
 275 280 285  
 Ala Gly Val Asn His Val Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly  
 290 295 300  
 Met Leu Thr Arg Leu Leu Leu Lys Ala Ser Asp Lys Ala Pro Trp Ser  
 305 310 315 320  
 Asp Asn Gly Asp Ala Lys Asn Pro Ala Leu Ser Pro Leu Gly Glu Asn  
 325 330 335  
 Val Lys Thr Lys Gly Gln Tyr Phe Tyr Gln Xaa Ala Leu Asp Gly Asn  
 340 345 350  
 Val Ala Gly Lys Glu Lys Gln Ala Leu Ile Asp Gln Phe Arg Ala Xaa  
 355 360 365  
 Gly Thr Gln Thr Tyr Ser Ala Thr Val Asn Val Tyr Gly Asn Lys Asp  
 370 375 380  
 Gly Lys Pro Asp Leu Asp Asn Ile Val Ala Thr Lys Lys Val Thr Ile  
 385 390 395 400  
 Asn Ile Asn Gly Leu Ile Ser Lys Glu Thr Val Gln Lys Ala Val Ala  
 405 410 415  
 Asp Asn Val Xaa Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu Glu Lys  
 420 425 430  
 Ala Lys Gly Glu Gly Pro Phe Thr Ala Gly Val Asn His Val Ile Pro  
 435 440 445  
 Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu Leu Lys  
 450 455 460  
 Ala Ser Asp Lys Ala Pro Trp Ser Asp Asn Gly Asp Ala Lys Asn Pro  
 465 470 475 480  
 Ala Leu Ser Pro Leu Gly Glu Asn Val Lys Thr Lys Gly Gln Tyr Phe  
 485 490 495  
 Tyr Gln Xaa Ala Leu Asp Gly Asn Val Ala Gly Lys Glu Lys Gln Ala  
 500 505 510  
 Leu Ile Asp Gln Phe Arg Ala Asn Gly Thr Gln Thr Tyr Ser Ala Thr  
 515 520 525  
 Val Asn Val Tyr Gly Asn Lys Asp Gly Lys Pro Asp Leu Asp Asn Ile  
 530 535 540  
 Val Ala Thr Lys Lys Val Thr Ile Lys Ile Asn Val Lys Glu Thr Ser  
 545 550 555 560  
 Asp Thr Ala Asn Gly Ser Leu Ser Pro Ser Asn Ser Gly Ser Gly Val  
 565 570 575  
 Thr Pro Met Asn His Asn His Ala Thr Gly Thr Thr Asp Ser Met Pro  
 580 585 590  
 Ala Asp Thr Met Thr Ser Ser Thr Asn Thr Met Ala Gly Glu Asn Met  
 595 600 605

Ala Ala Ser Ala Asn Lys Met Ser Asp Thr Met Met Ser Glu Asp Lys  
 610 615 620

Ala Met  
 625

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 593 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTCCAATCAA AAACAGGCAG ATGGTAAACT CAATATCGTG ACAACCTTTT ACCCTGTCTA  | 60  |
| TGA rTTTACC AAGCAAGTCG CAGGAGATAC GGCTAATGTA GAACTCCTAA TCGGTGCTGG | 120 |
| GACAGAACCT CATGAATACG AACCATCTGC CAAGGCAGTT GCCAAAATCC AAGATGCAGA  | 180 |
| TACCTTCGTT TATGAAAATG AAAACATGGA AACATGGGTA CCTAAATTGC TAGATACCTT  | 240 |
| GGATAAGAAA AAAGTGAAAA CCATCAAGGC GACAGGCGAT ATGTTGCTCT TGCCAGGTGG  | 300 |
| CGAGGAAGAA GAGGGAGACC ATGACCATGG AGAAGAAGGT CATCACCATG AGTTTGACCC  | 360 |
| CCATGTTTGG TTATCACCAG TTCGTGCCAT tAACTAGTA GAGCACCATC CGCGACACTT   | 420 |
| GTCAGCAGAT TATCCTGATA AAAAAGAGAC CTTTGAGAAG AATGCAGCTG CCTATATCGA  | 480 |
| AAAATTGCAA GCCTTGATA AGGCTTACGC AGAAGGTTTG TCTCAAGCAA AACAAAAGAG   | 540 |
| CTTTGTGACT CAACACGCAG CCTTTAACTa TCTTGCCTTG GACTATGGGA CTC         | 593 |

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 197 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

|                                                                 |           |
|-----------------------------------------------------------------|-----------|
| Ser Asn Gln Lys Gln Ala Asp Gly Lys Leu Asn Ile Val Thr Thr Phe | 1 5 10 15 |
| Tyr Pro Val Tyr Glu Phe Thr Lys Gln Val Ala Gly Asp Thr Ala Asn | 20 25 30  |
| Val Glu Leu Leu Ile Gly Ala Gly Thr Glu Pro His Glu Tyr Glu Pro | 35 40 45  |
| Ser Ala Lys Ala Val Ala Lys Ile Gln Asp Ala Asp Thr Phe Val Tyr | 50 55 60  |
| Glu Asn Glu Asn Met Glu Thr Trp Val Pro Lys Leu Leu Asp Thr Leu |           |

|                                                                 |     |    |     |    |     |     |
|-----------------------------------------------------------------|-----|----|-----|----|-----|-----|
| 65                                                              |     | 70 |     | 75 |     | 80  |
| Asp Lys Lys Lys Val Lys Thr Ile Lys Ala Thr Gly Asp Met Leu Leu | 85  |    | 90  |    | 95  |     |
| Leu Pro Gly Gly Glu Glu Glu Glu Gly Asp His Asp His Gly Glu Glu | 100 |    | 105 |    | 110 |     |
| Gly His His His Glu Phe Asp Pro His Val Trp Leu Ser Pro Val Arg | 115 |    | 120 |    | 125 |     |
| Ala Ile Lys Leu Val Glu His His Pro Arg His Leu Ser Ala Asp Tyr | 130 |    | 135 |    | 140 |     |
| Pro Asp Lys Lys Glu Thr Phe Glu Lys Asn Ala Ala Ala Tyr Ile Glu | 145 |    | 150 |    | 155 | 160 |
| Lys Leu Gln Ala Leu Asp Lys Ala Tyr Ala Glu Gly Leu Ser Gln Ala | 165 |    | 170 |    | 175 |     |
| Lys Gln Lys Ser Phe Val Thr Gln His Ala Ala Phe Asn Tyr Leu Ala | 180 |    | 185 |    | 190 |     |
| Leu Asp Tyr Gly Thr                                             | 195 |    |     |    |     |     |

## (2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1003 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TATCACAGGA TCGAACGGTA AGACAACCAC AACGACTATG ATTGGGGAAG TTTTGA CTGC | 60  |
| TGCTGGCCAA CATGGTCTTT TATCAGGGAA TATCGGCTAT CCAGCTAGTC AGGTGCTCA   | 120 |
| AATAGCATCA GATAAGGACA CGCTTGTTAT GGAAC TTTCT TCTTTCCAAC TCATGGGTGT | 180 |
| TCAAGAATTC CATCCAGAGA TTGCGGTTAT TACCAACCTC ATGCCAACTC ATATCGACTA  | 240 |
| CCATGGGTCA TTTTCGGAAT ATGTAGCAGC CAAGTGG AAT ATCCAGAACA AGATGACAGC | 300 |
| AGCTGATTC CTTGTCTTGA ACTTTAATCA AGACTTGGCA AAAGACTTGA CTTCCAAGAC   | 360 |
| AGAAGCCACT GTTG TACCAT TTTCAACACT TGAAAAGGTT GATGGAGCTT ATCTGGAAGA | 420 |
| TGGTCAACTC TACTTCCGTG GTGAAGTAGT CATGGCAGCG AATGAAATCG GTGTTCCAGG  | 480 |
| TAGCCACAAT GTGGAAAATG CCCTTGCGAC TATTGCTGTA GCCAAGCTTC GTGATGTGGA  | 540 |
| CAATCAAACC ATCAAGGAAA CTCTTTCAGC CTTCGGTGGT GTCAAACACC GTCTCCAGTT  | 600 |
| TGTGGATGAC ATCAAGGGTG TTAAATTCTA TAACGACAGT AAATCAACTA ATATCTTGGC  | 660 |
| TACTCAAAAA GCCTTGTCAG GATTTGACAA CAGCAAGGTC GTCTTGATTG CAGGTGGTTT  | 720 |
| GGACCGTGGC AATGAGTTTG ACGAATTGGT GCCAGACATT ACTGGACTCA AGAAGATGGT  | 780 |

CATCCTGGGT CAATCTGCAG AACGTGTCAA ACGGGCAGCA GACAAGGCTG GTGTCGCTTA 840  
 TGTGGAGGCG ACAGATATTG CAGATGCGAC CCGCAAGGCC TATGAGCTTG CGACTCAAGG 900  
 AGATGTGGTT CTTCTTAGTC CTGCCAATGC TAGCTGGGAT ATGTATGCTA ACTTTGAAGT 960  
 ACGTGGCGAC CTCTTTATCG ACACAGTAGC GGAGTTAAAA GAA 1003

## (2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 335 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Gly Ile Thr Gly Ser Asn Gly Lys Thr Thr Thr Thr Thr Met Ile Gly  
 1 5 10 15  
 Glu Val Leu Thr Ala Ala Gly Gln His Gly Leu Leu Ser Gly Asn Ile  
 20 25 30  
 Gly Tyr Pro Ala Ser Gln Val Ala Gln Ile Ala Ser Asp Lys Asp Thr  
 35 40 45  
 Leu Val Met Glu Leu Ser Ser Phe Gln Leu Met Gly Val Gln Glu Phe  
 50 55 60  
 His Pro Glu Ile Ala Val Ile Thr Asn Leu Met Pro Thr His Ile Asp  
 65 70 75 80  
 Tyr His Gly Ser Phe Ser Glu Tyr Val Ala Ala Lys Trp Asn Ile Gln  
 85 90 95  
 Asn Lys Met Thr Ala Ala Asp Phe Leu Val Leu Asn Phe Asn Gln Asp  
 100 105 110  
 Leu Ala Lys Asp Leu Thr Ser Lys Thr Glu Ala Thr Val Val Pro Phe  
 115 120 125  
 Ser Thr Leu Glu Lys Val Asp Gly Ala Tyr Leu Glu Asp Gly Gln Leu  
 130 135 140  
 Tyr Phe Arg Gly Glu Val Val Met Ala Ala Asn Glu Ile Gly Val Pro  
 145 150 155 160  
 Gly Ser His Asn Val Glu Asn Ala Leu Ala Thr Ile Ala Val Ala Lys  
 165 170 175  
 Leu Arg Asp Val Asp Asn Gln Thr Ile Lys Glu Thr Leu Ser Ala Phe  
 180 185 190  
 Gly Gly Val Lys His Arg Leu Gln Phe Val Asp Asp Ile Lys Gly Val  
 195 200 205  
 Lys Phe Tyr Asn Asp Ser Lys Ser Thr Asn Ile Leu Ala Thr Gln Lys  
 210 215 220  
 Ala Leu Ser Gly Phe Asp Asn Ser Lys Val Val Leu Ile Ala Gly Gly

|                                                                 |                         |                         |     |     |  |     |
|-----------------------------------------------------------------|-------------------------|-------------------------|-----|-----|--|-----|
| 225                                                             |                         | 230                     |     | 235 |  | 240 |
| Leu Asp Arg Gly                                                 | Asn Glu Phe Asp Glu     | Leu Val Pro Asp Ile Thr | Gly |     |  |     |
|                                                                 | 245                     | 250                     | 255 |     |  |     |
| Leu Lys Lys Met Val Ile Leu Gly                                 | Gln Ser Ala Glu Arg Val | Lys Arg                 |     |     |  |     |
|                                                                 | 260                     | 265                     | 270 |     |  |     |
| Ala Ala Asp Lys Ala Gly Val Ala Tyr Val Glu Ala Thr Asp Ile Ala |                         |                         |     |     |  |     |
|                                                                 | 275                     | 280                     | 285 |     |  |     |
| Asp Ala Thr Arg Lys Ala Tyr Glu Leu Ala Thr Gln Gly Asp Val Val |                         |                         |     |     |  |     |
|                                                                 | 290                     | 295                     | 300 |     |  |     |
| Leu Leu Ser Pro Ala Asn Ala Ser Trp Asp Met Tyr Ala Asn Phe Glu |                         |                         |     |     |  |     |
|                                                                 | 305                     | 310                     | 315 |     |  | 320 |
| Val Arg Gly Asp Leu Phe Ile Asp Thr Val Ala Glu Leu Lys Glu     |                         |                         |     |     |  |     |
|                                                                 | 325                     | 330                     | 335 |     |  |     |

## (2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 412 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| AAGTTCATCG AAGATGGTTG GGAAGTCCAC TATATCGGGG ACAAGTGTGG TATCGAACAC  | 60  |
| CAAGAAATCC TTAAGTCAGG TTTGGATGTC ACCTTCCATT CTATTGCGAC TGGAAAATTG  | 120 |
| CGTCGCTATT TCTCTTGGCA AAATATGCTG GACGTCTTCA AAGTTGGTTG GGGGAATTGTC | 180 |
| CAATCGCTCT TTATCATGTT GCGACTGCGT CCACAGACCC TTTTTTCAAA GGGGGGCTTT  | 240 |
| GTCTCAGTAC CGCTGTATAT CGCTGCGCGT GTGTCAGGAG TGCCTGTCTT TATTCACGAA  | 300 |
| TCTGACCTGT CTATGGGCTT GGCCAATAAA ATCGCCTATA AATTGCGAC TAAGATGTAT   | 360 |
| TCAACCTTTG AACAAGCTTC GAGTTTGGCT AAGGTTGAGC ATGTGGGAGC GG          | 412 |

## (2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

|                                                                 |    |   |    |    |  |  |  |    |  |
|-----------------------------------------------------------------|----|---|----|----|--|--|--|----|--|
| Ser Ser Ser Lys Met Val Gly Lys Ser Thr Ile Ser Gly Thr Ser Val |    |   |    |    |  |  |  |    |  |
| 1                                                               |    | 5 |    | 10 |  |  |  | 15 |  |
| Val Ser Asn Thr Lys Lys Ser Leu Ser Gln Val Trp Met Ser Pro Ser |    |   |    |    |  |  |  |    |  |
|                                                                 | 20 |   | 25 |    |  |  |  | 30 |  |

Ile Leu Leu Arg Leu Glu Asn Cys Val Ala Ile Ser Leu Gly Lys Ile  
                   35                  40                  45  
 Cys Trp Thr Ser Ser Lys Leu Val Gly Glu Leu Ser Asn Arg Ser Leu  
           50                  55                  60  
 Ser Cys Cys Asp Cys Val His Arg Pro Phe Phe Gln Arg Gly Ala Leu  
   65                  70                  75                  80  
 Ser Gln Tyr Arg Leu Leu Ser Leu Arg Val Cys Gln Glu Cys Leu Ser  
                   85                  90                  95  
 Leu Phe Thr Asn Leu Thr Cys Leu Trp Ala Trp Pro Ile Lys Ser Pro  
                   100                  105                  110  
 Ile Asn Leu Arg Leu Arg Cys Ile Gln Pro Leu Asn Lys Leu Arg Val  
           115                  120                  125  
 Trp Leu Arg Leu Ser Met Trp Glu Arg  
       130                  135

## (2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 544 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATCGCTAGCT AGTGAAATGC AAGAAAGTAC ACGTAAATTC AAGGTTACTG CTGACCTAAC | 60  |
| AGATGCCGGT GTTGAACGA TTGAAGTTCC TTTGAGCATT GAAGATTTAC CCAATGGGCT  | 120 |
| GACCGCTGTG GCGACTCCGC AAAAAATTAC AGTCAAGATT GGTAAGAAGG CTCAGAAGGA | 180 |
| TAAGGTAAAG ATTGTACCAG AGATTGACCC TAGTCAAATT GATAGTCGGG TACAAATTGA | 240 |
| AAATGTCATG GTGTCAGATA AAGAAGTGTC TATTACGAGT GACCAAGAGA CATTGGATAG | 300 |
| AATTGATAAG ATTATCGCTG TTTTGCCAAC TAGCGAACGT ATAACAGGTA ATTACAGTGG | 360 |
| TTCAGTACCT TTGCAGGCAA TCGACCGCAA TGGTGTTGTC TTACCGGCAG TTATCACTCC | 420 |
| GTTTGATACA ATAATGAAGG TGACTACAAA ACCAGTAGCA CCAAGTTCAA GCACATCAAA | 480 |
| TTCAAGTACA AGCAGTTCAT CGGAGACATC TTCGTCAACG AAAGCAACTA GTTCAAAAAC | 540 |
| GAAT                                                              | 544 |

## (2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 181 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Ser Leu Ala Ser Glu Met Gln Glu Ser Thr Arg Lys Phe Lys Val Thr  
 1 5 10 15  
 Ala Asp Leu Thr Asp Ala Gly Val Gly Thr Ile Glu Val Pro Leu Ser  
 20 25 30  
 Ile Glu Asp Leu Pro Asn Gly Leu Thr Ala Val Ala Thr Pro Gln Lys  
 35 40 45  
 Ile Thr Val Lys Ile Gly Lys Lys Ala Gln Lys Asp Lys Val Lys Ile  
 50 55 60  
 Val Pro Glu Ile Asp Pro Ser Gln Ile Asp Ser Arg Val Gln Ile Glu  
 65 70 75 80  
 Asn Val Met Val Ser Asp Lys Glu Val Ser Ile Thr Ser Asp Gln Glu  
 85 90 95  
 Thr Leu Asp Arg Ile Asp Lys Ile Ile Ala Val Leu Pro Thr Ser Glu  
 100 105 110  
 Arg Ile Thr Gly Asn Tyr Ser Gly Ser Val Pro Leu Gln Ala Ile Asp  
 115 120 125  
 Arg Asn Gly Val Val Leu Pro Ala Val Ile Thr Pro Phe Asp Thr Ile  
 130 135 140  
 Met Lys Val Thr Thr Lys Pro Val Ala Pro Ser Ser Ser Thr Ser Asn  
 145 150 155 160  
 Ser Ser Thr Ser Ser Ser Ser Glu Thr Ser Ser Ser Thr Lys Ala Thr  
 165 170 175  
 Ser Ser Lys Thr Asn  
 180

## (2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1267 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GCACCAGATG GGGCACAAGG TTCAGGGATC AGATGTTGAA AAGTACTACT TTACCCAACG 60  
 CGGTCTTGAG CAGGCAGGAA TTACCATCTT TCCTTTTGAT GAAAAAATC TAGACGGTGA 120  
 TATGGAAATT ATCGCTGGAA ATGCCCTTTCG TCCAGATAAC AACGTCGAAA TTGCCTATGC 180  
 GGACCAAAAT GGTATCAGCT ACAAACGTTA CCATGAGTTT CTAGGTAGCT TTATGCGTGA 240  
 CTTTGTTAGC ATGGGAGTAG CAGGAGCACA TGGAAAACT TCAACGACAG GTATGTTGTC 300  
 TCATGTCTTG TCTCACATTA CAGATACCAG CTTCTTGATT GGAGATGGGA CAGGTCGTGG 360  
 TTCGGCCAAT GCCAAATATT TTGTCTTTGA ATCTGACGAA TATGAGCGTC ACTTCATGCC 420

```

TTACCACCCA GAATACTCTA TTATCACCAA CATTGACTTT GACCATCCAG ATTATTTTAC      480
AAGTCTCGAG GATGTTTTTA ATGCCTTTAA CGACTATGCC AAACAAATCA CCAAGGGTCT      540
TTTTGTCTAT GGTGAAGATG CTGAATTGCG TAAGATTACG TCTGATGCAC CAATTTATTA      600
TTATGGTTTT GAAGCTGAAG GCAATGACTT TGTAGCTAGT GATCTTCTTC GTTCAATAAC      660
TGGTTCAACC TTCACCGTTC ATTTCCGTGG ACAAACCTTG GGGCAATTCC ACATTCCAAC      720
CTTTGGTCGT CACAATATCA TGAATGCGAC AGCCGTTATT GGTCTTCTTT ACACAGCAGG      780
ATTTGATTTG AACTTGGTGC GTGAGCACTT GAAAACATTT GCCGGTGTTA AACGTCGTTT      840
CACTGAGAAA ATTGTCAATG ATACAGTGAT TATCGATGAC TTTGCCCCACC ATCCAACAGA      900
AATTATTGCG ACCTTGGATG CGGCTCGTCA GAAATACCCA AGCAAGGAAA TTGTAGCAGT      960
CTTTCAACCG CATACTTTA CAAGAACCAT TGCCTTGTTG GACGACTTTG CCCATGCTTT     1020
AAACCAAGCA GATGCTGTTT ATCTAGCGCA AATTTATGGC TCGGCTCGTG AAGTAGATCA     1080
TGGTGACGTT AAGGTAGAAG ACCTAGCCAA CAAAATCAAC AAAAAACACC AAGTGATTAC     1140
TGTTGAAAAT GTTTCTCCAC TCCTAGACCA TGACAATGCT GTTTACGTCT TTATGGGAGC     1200
AGGAGACATC CAAACCTATG AATACTCATT TGAGCGTCTC TTGTCTAACT TGACAAGCAA     1260
TGTTCAA   1267

```

## (2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 422 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```

His Gln Met Gly His Lys Val Gln Gly Ser Asp Val Glu Lys Tyr Tyr
1           5           10
Phe Thr Gln Arg Gly Leu Glu Gln Ala Gly Ile Thr Ile Leu Pro Phe
20        25        30
Asp Glu Lys Asn Leu Asp Gly Asp Met Glu Ile Ile Ala Gly Asn Ala
35        40        45
Phe Arg Pro Asp Asn Asn Val Glu Ile Ala Tyr Ala Asp Gln Asn Gly
50        55        60
Ile Ser Tyr Lys Arg Tyr His Glu Phe Leu Gly Ser Phe Met Arg Asp
65        70        75        80
Phe Val Ser Met Gly Val Ala Gly Ala His Gly Lys Thr Ser Thr Thr
85        90        95
Gly Met Leu Ser His Val Leu Ser His Ile Thr Asp Thr Ser Phe Leu
100       105       110

```

Ile Gly Asp Gly Thr Gly Arg Gly Ser Ala Asn Ala Lys Tyr Phe Val  
           115                                  120                                  125  
 Phe Glu Ser Asp Glu Tyr Glu Arg His Phe Met Pro Tyr His Pro Glu  
           130                                  135                                  140  
 Tyr Ser Ile Ile Thr Asn Ile Asp Phe Asp His Pro Asp Tyr Phe Thr  
           145                                  150                                  155                                  160  
 Ser Leu Glu Asp Val Phe Asn Ala Phe Asn Asp Tyr Ala Lys Gln Ile  
                                   165                                  170                                  175  
 Thr Lys Gly Leu Phe Val Tyr Gly Glu Asp Ala Glu Leu Arg Lys Ile  
                                   180                                  185                                  190  
 Thr Ser Asp Ala Pro Ile Tyr Tyr Tyr Gly Phe Glu Ala Glu Gly Asn  
                                   195                                  200                                  205  
 Asp Phe Val Ala Ser Asp Leu Leu Arg Ser Ile Thr Gly Ser Thr Phe  
           210                                  215                                  220  
 Thr Val His Phe Arg Gly Gln Asn Leu Gly Gln Phe His Ile Pro Thr  
           225                                  230                                  235                                  240  
 Phe Gly Arg His Asn Ile Met Asn Ala Thr Ala Val Ile Gly Leu Leu  
                                   245                                  250                                  255  
 Tyr Thr Ala Gly Phe Asp Leu Asn Leu Val Arg Glu His Leu Lys Thr  
                                   260                                  265                                  270  
 Phe Ala Gly Val Lys Arg Arg Phe Thr Glu Lys Ile Val Asn Asp Thr  
                                   275                                  280                                  285  
 Val Ile Ile Asp Asp Phe Ala His His Pro Thr Glu Ile Ile Ala Thr  
           290                                  295                                  300  
 Leu Asp Ala Ala Arg Gln Lys Tyr Pro Ser Lys Glu Ile Val Ala Val  
           305                                  310                                  315                                  320  
 Phe Gln Pro His Thr Phe Thr Arg Thr Ile Ala Leu Leu Asp Asp Phe  
                                   325                                  330                                  335  
 Ala His Ala Leu Asn Gln Ala Asp Ala Val Tyr Leu Ala Gln Ile Tyr  
                                   340                                  345                                  350  
 Gly Ser Ala Arg Glu Val Asp His Gly Asp Val Lys Val Glu Asp Leu  
                                   355                                  360                                  365  
 Ala Asn Lys Ile Asn Lys Lys His Gln Val Ile Thr Val Glu Asn Val  
           370                                  375                                  380  
 Ser Pro Leu Leu Asp His Asp Asn Ala Val Tyr Val Phe Met Gly Ala  
           385                                  390                                  395                                  400  
 Gly Asp Ile Gln Thr Tyr Glu Tyr Ser Phe Glu Arg Leu Leu Ser Asn  
                                   405                                  410                                  415  
 Leu Thr Ser Asn Val Gln  
                                   420

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TTTTAACCCA ACTGTTGGTA CTTTCCTTTT TACTGCAGGA TTGAGCTTGT TAGTTTTATT  | 60   |
| GGTTTCTAAA AGGGAAAATG GAAAGAAACG ACTTGTTTCAT TTTCTGCTGT TGACTAGCAT | 120  |
| GGGAGTTCAA TTGTTGCCGG CCAGTGCTTT TGGGTTGACC AGCCAGATTT TATCTGCCTA  | 180  |
| TAATAGTCAG CTTTCTATCG GAGTCGGGGA ACATTTACCA GAGCCTCTGA AAATCGAAGG  | 240  |
| TTATCAATAT ATTGGTTATA TCAAACTAA GAAACAGGAT AATACAGAGC TTTCAAGGAC   | 300  |
| AGTTGATGGG AAATACTCTG CTCAAAGAGA TAGTCAACCA AACTCTACAA AAACATCAGA  | 360  |
| TGTAGTTCAT TCAGCTGATT TAGAATGGAA CCAAGGACAG GGAAGGTTA GTTTACAAGG   | 420  |
| TGAAGCATCA GGGGATGATG GACTTTCAGA AAAATCTTCT ATAGCAGCAG ACAATCTATC  | 480  |
| TTCTAATGAT TCATTGCAA GTCAAGTTGA GCAGAATCCG GATCACAAAG GAGAATCTGT   | 540  |
| AGTTGACCA ACAGTGCCAG AACAAGGAAA TCCTGTGTCT GCTACAACGG TGCAGAGTGC   | 600  |
| GGAAGAGGAA GTATTGGCGA CGACAAATGA TCGACCAGAG TATAAACTTC CATTGGAAAC  | 660  |
| CAAAGGCACG CAAGAACCCG GTCATGAGGG TGAAGCCGCA GTCCGTGAAG ACTTACCAGT  | 720  |
| CTACACTAAG CCACTAGAAA CCAAAGGTAC ACAAGGACCC GGACATGAAG GTGAAGCTGC  | 780  |
| AGTTCGCGAG GAAGAACCAG CTTACACAGA ACCGTTAGCA ACGAAAGGCA CGCAAGAGCC  | 840  |
| AGGTCATGAG GGCAAAGCTA CAGTCCGCGA AGAGACTCTA GAGTACACGG AACCGGTAGC  | 900  |
| GACAAAAGGC ACACAAGAAC CCGAACATGA GGGCGAaCGG sCAGTAGAAG AAGAACTTCC  | 960  |
| GGCTTTAGAG GTCACTACAC GAAATAGAAC GGAAATCCAG AATATTCCTT ATACAACAGA  | 1020 |
| AGAAATTCAG GATCCAACAC TTCTGAAAAA TCGTCGTAAG ATTGAACGAC AAGGGCAAGC  | 1080 |
| AGGGACACGT ACAATTCAAT ATGAAGACTA CATCGTAAAT GGTAATGTCG TAGAAACTAA  | 1140 |
| AGAAGTGTCA CGAACTGAAG TAGCTCCGGT CAACGAAGTC GTTAAAGTAG GAACACTTGT  | 1200 |
| GAAAGTTAAA CCTACAGTAG AAATTACAAA CTTAACAAAA GTTGAGAACA AAAAATCTAT  | 1260 |
| AACTGTAAGT TATAACTTAA TAGACACTAC CTCAGCATAT GTTTCTGCAA AAACGCAAGT  | 1320 |
| TTTCCATGGA GACAAGCTAG TTAAAGAGGT GGATATAGAA AATCCTGCCA AAGAGCAAGT  | 1380 |
| AATATCAGGT TTAGATTACT ACACACCGTA TACAGTTAAA ACACACCTAA CTTATAATTT  | 1440 |
| GGGTGAAAAT AATGAGGAAA ATACTGAAAC ATCAACTCAA GATTTCCAAT TAGAGTATAA  | 1500 |
| GAAAATAGAG ATTAAAGATA TTGATTCACT AGAATTATAC GGTAAAGAAA ATGATCGTTA  | 1560 |
| TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAGT  | 1620 |
| GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA  | 1680 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TGGAACGTAT AAAGTGACGG TAGCCGTTGA TCAACTTGTC GAAGAAGGTA CAGACGGTTA  | 1740 |
| CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC  | 1800 |
| ATCCTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC  | 1860 |
| TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCGATAAG CAGACAAGTT ATCTCACAGG  | 1920 |
| TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAAA TCGTATGCCA TTTATGATTT  | 1980 |
| GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAAAAAC | 2040 |
| TGTTTCTGCT GATAGTAAAG AAAATGTCGC AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA  | 2100 |
| TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT  | 2160 |
| AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA  | 2220 |
| TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG  | 2280 |
| TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA  | 2340 |
| CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT  | 2400 |
| TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC  | 2460 |
| TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA  | 2520 |
| TGTTATCACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA  | 2580 |
| TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT  | 2640 |
| TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT  | 2700 |
| AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG  | 2760 |
| CAACATAGAA AACTGATGC CATTCTACAA TAAAGACCTA GTAGTTCACT ATGGTAACAA   | 2820 |
| AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTTA GATGTTGTGC CGATGAAAGA  | 2880 |
| TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA  | 2940 |
| TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TCAATAACAG   | 3000 |
| TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT  | 3060 |
| TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA  | 3120 |
| C                                                                  | 3121 |

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu  
 1 5 10 15  
 Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val  
 20 25 30  
 His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser  
 35 40 45  
 Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu  
 50 55 60  
 Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly  
 65 70 75 80  
 Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu  
 85 90 95  
 Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln  
 100 105 110  
 Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu  
 115 120 125  
 Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly  
 130 135 140  
 Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser  
 145 150 155 160  
 Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys  
 165 170 175  
 Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val  
 180 185 190  
 Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr  
 195 200 205  
 Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln  
 210 215 220  
 Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val  
 225 230 235 240  
 Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu  
 245 250 255  
 Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu  
 260 265 270  
 Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val  
 275 280 285  
 Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr  
 290 295 300  
 Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro  
 305 310 315 320  
 Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro  
 325 330 335  
 Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg

| 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ile | Glu | Arg | Gln | Gly | Gln | Ala | Gly | Thr | Arg | Thr | Ile | Gln | Tyr | Glu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Asp | Tyr | Ile | Val | Asn | Gly | Asn | Val | Val | Glu | Thr | Lys | Glu | Val | Ser | Arg |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Thr | Glu | Val | Ala | Pro | Val | Asn | Glu | Val | Val | Lys | Val | Gly | Thr | Leu | Val |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Lys | Val | Lys | Pro | Thr | Val | Glu | Ile | Thr | Asn | Leu | Thr | Lys | Val | Glu | Asn |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Lys | Lys | Ser | Ile | Thr | Val | Ser | Tyr | Asn | Leu | Ile | Asp | Thr | Thr | Ser | Ala |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Tyr | Val | Ser | Ala | Lys | Thr | Gln | Val | Phe | His | Gly | Asp | Lys | Leu | Val | Lys |
|     |     |     | 435 |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Glu | Val | Asp | Ile | Glu | Asn | Pro | Ala | Lys | Glu | Gln | Val | Ile | Ser | Gly | Leu |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Asp | Tyr | Tyr | Thr | Pro | Tyr | Thr | Val | Lys | Thr | His | Leu | Thr | Tyr | Asn | Leu |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Gly | Glu | Asn | Asn | Glu | Glu | Asn | Thr | Glu | Thr | Ser | Thr | Gln | Asp | Phe | Gln |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Leu | Glu | Tyr | Lys | Lys | Ile | Glu | Ile | Lys | Asp | Ile | Asp | Ser | Val | Glu | Leu |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Tyr | Gly | Lys | Glu | Asn | Asp | Arg | Tyr | Arg | Arg | Tyr | Leu | Ser | Leu | Ser | Glu |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Ala | Pro | Thr | Asp | Thr | Ala | Lys | Tyr | Phe | Val | Lys | Val | Lys | Ser | Asp | Arg |
|     |     | 530 |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Phe | Lys | Glu | Met | Tyr | Leu | Pro | Val | Lys | Ser | Ile | Thr | Glu | Asn | Thr | Asp |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Gly | Thr | Tyr | Lys | Val | Thr | Val | Ala | Val | Asp | Gln | Leu | Val | Glu | Glu | Gly |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Thr | Asp | Gly | Tyr | Lys | Asp | Asp | Tyr | Thr | Phe | Thr | Val | Ala | Lys | Ser | Lys |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Ala | Glu | Gln | Pro | Gly | Val | Tyr | Thr | Ser | Phe | Lys | Gln | Leu | Val | Thr | Ala |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Met | Gln | Ser | Asn | Leu | Ser | Gly | Val | Tyr | Thr | Leu | Ala | Ser | Asp | Met | Thr |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Ala | Asp | Glu | Val | Ser | Leu | Gly | Asp | Lys | Gln | Thr | Ser | Tyr | Leu | Thr | Gly |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |
| Ala | Phe | Thr | Gly | Ser | Leu | Ile | Gly | Ser | Asp | Gly | Thr | Lys | Ser | Tyr | Ala |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |
| Ile | Tyr | Asp | Leu | Lys | Lys | Pro | Leu | Phe | Asp | Thr | Leu | Asn | Gly | Ala | Thr |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |
| Val | Arg | Asp | Leu | Asp | Ile | Lys | Thr | Val | Ser | Ala | Asp | Ser | Lys | Glu | Asn |
|     |     |     | 675 |     |     |     | 680 |     |     |     |     | 685 |     |     |     |

Val Ala Ala Leu Ala Lys Ala Ala Asn Ser Ala Asn Ile Asn Asn Val  
 690 695 700  
 Ala Val Glu Gly Lys Ile Ser Gly Ala Lys Ser Val Ala Gly Leu Val  
 705 710 715 720  
 Ala Ser Ala Thr Asn Thr Val Ile Glu Asn Ser Ser Phe Thr Gly Lys  
 725 730 735  
 Leu Ile Ala Asn His Gln Asp Ser Asn Lys Asn Asp Thr Gly Gly Ile  
 740 745 750  
 Val Gly Asn Ile Thr Gly Asn Ser Ser Arg Val Asn Lys Val Arg Val  
 755 760 765  
 Asp Ala Leu Ile Ser Thr Asn Ala Arg Asn Asn Asn Gln Thr Ala Gly  
 770 775 780  
 Gly Ile Val Gly Arg Leu Glu Asn Gly Ala Leu Ile Ser Asn Ser Val  
 785 790 795 800  
 Ala Thr Gly Glu Ile Arg Asn Gly Gln Gly Tyr Ser Arg Val Gly Gly  
 805 810 815  
 Ile Val Gly Ser Thr Trp Gln Asn Gly Arg Val Asn Asn Val Val Ser  
 820 825 830  
 Asn Val Asp Val Gly Asp Gly Tyr Val Ile Thr Gly Asp Gln Tyr Ala  
 835 840 845  
 Ala Ala Asp Val Lys Asn Ala Ser Thr Ser Val Asp Asn Arg Lys Ala  
 850 855 860  
 Asp Arg Phe Ala Thr Lys Leu Ser Lys Asp Gln Ile Asp Ala Lys Val  
 865 870 875 880  
 Ala Asp Tyr Gly Ile Thr Val Thr Leu Asp Asp Thr Gly Gln Asp Leu  
 885 890 895  
 Lys Arg Asn Leu Arg Glu Val Asp Tyr Thr Arg Leu Asn Lys Ala Glu  
 900 905 910  
 Ala Glu Arg Lys Val Ala Tyr Ser Asn Ile Glu Lys Leu Met Pro Phe  
 915 920 925  
 Tyr Asn Lys Asp Leu Val Val His Tyr Gly Asn Lys Val Ala Thr Thr  
 930 935 940  
 Asp Lys Leu Tyr Thr Thr Glu Leu Leu Asp Val Val Pro Met Lys Asp  
 945 950 955 960  
 Asp Glu Val Val Thr Asp Ile Asn Asn Lys Lys Asn Ser Ile Asn Lys  
 965 970 975  
 Val Met Leu His Phe Lys Asp Asn Thr Val Glu Tyr Leu Asp Val Thr  
 980 985 990  
 Phe Lys Glu Asn Phe Ile Asn Ser Gln Val Ile Glu Tyr Asn Val Thr  
 995 1000 1005  
 Gly Lys Glu Tyr Ile Phe Thr Pro Glu Ala Phe Val Ser Asp Tyr Thr  
 1010 1015 1020

Ala Ile Thr Asn Asn Val Leu Ser Asp Leu Gln Asn Val Thr Leu Asn  
 1025 1030 1035 1040

## (2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1567 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TTTTAACCCA ACTGTTGGTA CTTTCCTTTT TACTGCAGGA TTGAGCTTGT TAGTTTTATT  | 60   |
| GGTTTCTAAA AGGGAAAATG GAAAGAAACG ACTTGTTTCAT TTTCTGCTGT TGACTAGCAT | 120  |
| GGGAGTTCAA TTGTTGCCGG CCAGTGCTTT TGGGTTGACC AGCCAGATTT TATCTGCCTA  | 180  |
| TAATAGTCAG CTTTCTATCG GAGTCGGGGA ACATTACCA GAGCCTCTGA AAATCGAAGG   | 240  |
| TTATCAATAT ATTGTTTATA TCAAACTAA GAAACAGGAT AATACAGAGC TTTCAAGGAC   | 300  |
| AGTTGATGGG AAATACTCTG CTCAAAGAGA TAGTCAACCA AACTCTACAA AAACATCAGA  | 360  |
| TGTAGTTCAT TCAGCTGATT TAGAATGGAA CCAAGGACAG GGGAAGGTTA GTTTACAAGG  | 420  |
| TGAAGCATCA GGGGATGATG GACTTTCAGA AAAATCTTCT ATAGCAGCAG ACAATCTATC  | 480  |
| TTCTAATGAT TCATTGCAA GTCAAGTTGA GCAGAATCCG GATCACAAAG GAGAATCTGT   | 540  |
| AGTTGACCA ACAGTGCCAG AACAAAGGAAA TCCTGTGTCT GCTACAACGG TGCAGAGTGC  | 600  |
| GGAAGAGGAA GTATTGGCGA CGACAAATGA TCGACCAGAG TATAAACTTC CATTGGAAAC  | 660  |
| CAAAGGCACG CAAGAACCCG GTCATGAGGG TGAAGCCGCA GTCCGTGAAG ACTTACCAGT  | 720  |
| CTACACTAAG CCACTAGAAA CCAAAGGTAC ACAAGGACCC GGACATGAAG GTGAAGCTGC  | 780  |
| AGTTGCGGAG GAAGAACCAG CTTACACAGA ACCGTTAGCA ACGAAAGGCA CGCAAGAGCC  | 840  |
| AGGTCATGAG GGCAAAGCTA CAGTCCGCGA AGAGACTCTA GAGTACACGG AACCGGTAGC  | 900  |
| GACAAAAGGC ACACAAGAAC CCGAACATGA GGGCGAaCGG sCAGTAGAAG AAGAACTTCC  | 960  |
| GGCTTTAGAG GTCACTACAC GAAATAGAAC GGAAATCCAG AATATTCCTT ATACAACAGA  | 1020 |
| AGAAATTCAG GATCCAACAC TTCTGAAAAA TCGTCGTAAG ATTGAACGAC AAGGGCAAGC  | 1080 |
| AGGGACACGT ACAATTCAAT ATGAAGACTA CATCGTAAAT GGTAATGTCG TAGAACTAA   | 1140 |
| AGAAGTGTC ACGAACTGAAG TAGCTCCGGT CAACGAAGTC GTTAAAGTAG GAACACTTGT  | 1200 |
| GAAAGTTAAA CCTACAGTAG AAATTACAAA CTTAACAAAA GTTGAGAACA AAAAATCTAT  | 1260 |
| AACTGTAAGT TATAACTTAA TAGACACTAC CTCAGCATAT GTTCTTGCAA AAACGCAAGT  | 1320 |
| TTTCCATGGA GACAAGCTAG TTAAAGAGGT GGATATAGAA AATCCTGCCA AAGAGCAAGT  | 1380 |
| AATATCAGGT TTAGATTACT ACACACCGTA TACAGTTAAA ACACACCTAA CTTATAATTT  | 1440 |
| GGGTGAAAAT AATGAGGAAA ATACTGAAAC ATCAACTCAA GATTTCCAAT TAGAGTATAA  | 1500 |

GAAAATAGAG ATTAAAGATA TTGATTCAGT AGAATTATAC GGTAAGAAA ATGATCGTTA 1560  
TCGTAGA 1567

## (2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 522 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Asn | Pro | Thr | Val | Gly | Thr | Phe | Leu | Phe | Thr | Ala | Gly | Leu | Ser | Leu | 1   | 5   | 10  | 15  |
| Leu | Val | Leu | Leu | Val | Ser | Lys | Arg | Glu | Asn | Gly | Lys | Lys | Arg | Leu | Val | 20  | 25  | 30  |     |
| His | Phe | Leu | Leu | Thr | Ser | Met | Gly | Val | Gln | Leu | Leu | Pro | Ala | Ser | 35  | 40  | 45  |     |     |
| Ala | Phe | Gly | Leu | Thr | Ser | Gln | Ile | Leu | Ser | Ala | Tyr | Asn | Ser | Gln | Leu | 50  | 55  | 60  |     |
| Ser | Ile | Gly | Val | Gly | Glu | His | Leu | Pro | Glu | Pro | Leu | Lys | Ile | Glu | Gly | 65  | 70  | 75  | 80  |
| Tyr | Gln | Tyr | Ile | Gly | Tyr | Ile | Lys | Thr | Lys | Lys | Gln | Asp | Asn | Thr | Glu | 85  | 90  | 95  |     |
| Leu | Ser | Arg | Thr | Val | Asp | Gly | Lys | Tyr | Ser | Ala | Gln | Arg | Asp | Ser | Gln | 100 | 105 | 110 |     |
| Pro | Asn | Ser | Thr | Lys | Thr | Ser | Asp | Val | Val | His | Ser | Ala | Asp | Leu | Glu | 115 | 120 | 125 |     |
| Trp | Asn | Gln | Gly | Gln | Gly | Lys | Val | Ser | Leu | Gln | Gly | Glu | Ala | Ser | Gly | 130 | 135 | 140 |     |
| Asp | Asp | Gly | Leu | Ser | Glu | Lys | Ser | Ser | Ile | Ala | Ala | Asp | Asn | Leu | Ser | 145 | 150 | 155 | 160 |
| Ser | Asn | Asp | Ser | Phe | Ala | Ser | Gln | Val | Glu | Gln | Asn | Pro | Asp | His | Lys | 165 | 170 | 175 |     |
| Gly | Glu | Ser | Val | Val | Arg | Pro | Thr | Val | Pro | Glu | Gln | Gly | Asn | Pro | Val | 180 | 185 | 190 |     |
| Ser | Ala | Thr | Thr | Val | Gln | Ser | Ala | Glu | Glu | Glu | Val | Leu | Ala | Thr | Thr | 195 | 200 | 205 |     |
| Asn | Asp | Arg | Pro | Glu | Tyr | Lys | Leu | Pro | Leu | Glu | Thr | Lys | Gly | Thr | Gln | 210 | 215 | 220 |     |
| Glu | Pro | Gly | His | Glu | Gly | Glu | Ala | Ala | Val | Arg | Glu | Asp | Leu | Pro | Val | 225 | 230 | 235 | 240 |
| Tyr | Thr | Lys | Pro | Leu | Glu | Thr | Lys | Gly | Thr | Gln | Gly | Pro | Gly | His | Glu |     |     |     |     |

| 245 |     |     |     |     |     |     |     |     |     | 250 |     |     | 255 |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Gly | Glu | Ala | Ala | Val | Arg | Glu | Glu | Glu | Pro | Ala | Tyr | Thr | Glu | Pro | Leu |  |  |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |  |  |
| Ala | Thr | Lys | Gly | Thr | Gln | Glu | Pro | Gly | His | Glu | Gly | Lys | Ala | Thr | Val |  |  |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |  |  |
| Arg | Glu | Glu | Thr | Leu | Glu | Tyr | Thr | Glu | Pro | Val | Ala | Thr | Lys | Gly | Thr |  |  |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |  |  |
| Gln | Glu | Pro | Glu | His | Glu | Gly | Glu | Arg | Xaa | Val | Glu | Glu | Glu | Leu | Pro |  |  |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |  |  |
| Ala | Leu | Glu | Val | Thr | Thr | Arg | Asn | Arg | Thr | Glu | Ile | Gln | Asn | Ile | Pro |  |  |  |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |  |  |
| Tyr | Thr | Thr | Glu | Glu | Ile | Gln | Asp | Pro | Thr | Leu | Leu | Lys | Asn | Arg | Arg |  |  |  |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |  |  |
| Lys | Ile | Glu | Arg | Gln | Gly | Gln | Ala | Gly | Thr | Arg | Thr | Ile | Gln | Tyr | Glu |  |  |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |  |  |
| Asp | Tyr | Ile | Val | Asn | Gly | Asn | Val | Val | Glu | Thr | Lys | Glu | Val | Ser | Arg |  |  |  |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |  |  |
| Thr | Glu | Val | Ala | Pro | Val | Asn | Glu | Val | Val | Lys | Val | Gly | Thr | Leu | Val |  |  |  |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |  |  |
| Lys | Val | Lys | Pro | Thr | Val | Glu | Ile | Thr | Asn | Leu | Thr | Lys | Val | Glu | Asn |  |  |  |  |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |  |  |  |
| Lys | Lys | Ser | Ile | Thr | Val | Ser | Tyr | Asn | Leu | Ile | Asp | Thr | Thr | Ser | Ala |  |  |  |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |  |  |
| Tyr | Val | Ser | Ala | Lys | Thr | Gln | Val | Phe | His | Gly | Asp | Lys | Leu | Val | Lys |  |  |  |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |  |  |
| Glu | Val | Asp | Ile | Glu | Asn | Pro | Ala | Lys | Glu | Gln | Val | Ile | Ser | Gly | Leu |  |  |  |  |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |  |  |  |
| Asp | Tyr | Tyr | Thr | Pro | Tyr | Thr | Val | Lys | Thr | His | Leu | Thr | Tyr | Asn | Leu |  |  |  |  |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |  |  |  |
| Gly | Glu | Asn | Asn | Glu | Glu | Asn | Thr | Glu | Thr | Ser | Thr | Gln | Asp | Phe | Gln |  |  |  |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |  |  |  |  |
| Leu | Glu | Tyr | Lys | Lys | Ile | Glu | Ile | Lys | Asp | Ile | Asp | Ser | Val | Glu | Leu |  |  |  |  |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |  |  |  |  |
| Tyr | Gly | Lys | Glu | Asn | Asp | Arg | Tyr | Arg | Arg |     |     |     |     |     |     |  |  |  |  |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     |     |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1561 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAAGT | 60   |
| GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA  | 120  |
| TGGAACGTAT AAAGTGACGG TAGCCGTTGA TCAACTTGTC GAAGAAGGTA CAGACGGTTA  | 180  |
| CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC  | 240  |
| ATCCTTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC | 300  |
| TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCGATAAG CAGACAAGTT ATCTCACAGG  | 360  |
| TGCATTTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAAA TCGTATGCCA TTTATGATTT | 420  |
| GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAAAAAC | 480  |
| TGTTTCTGCT GATAGTAAAG AAAATGTGCG AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA  | 540  |
| TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT  | 600  |
| AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA  | 660  |
| TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG  | 720  |
| TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA  | 780  |
| CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT  | 840  |
| TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC  | 900  |
| TACGTGGCAA AACGGTTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA | 960  |
| TGTTATCACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA  | 1020 |
| TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT  | 1080 |
| TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT  | 1140 |
| AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG  | 1200 |
| CAACATAGAA AAATGATGC CATTCTACAA TAAAGACCTA GTAGTTCACT ATGGTAACAA   | 1260 |
| AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTTA GATGTTGTGC CGATGAAAGA  | 1320 |
| TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA  | 1380 |
| TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TCATAAACAG   | 1440 |
| TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT  | 1500 |
| TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA  | 1560 |
| C                                                                  | 1561 |

## (2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 520 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Arg | Tyr | Leu | Ser | Leu | Ser | Glu | Ala | Pro | Thr | Asp | Thr | Ala | Lys | Tyr | 1   | 5   | 10  | 15  |
| Phe | Val | Lys | Val | Lys | Ser | Asp | Arg | Phe | Lys | Glu | Met | Tyr | Leu | Pro | Val | 20  | 25  | 30  |     |
| Lys | Ser | Ile | Thr | Glu | Asn | Thr | Asp | Gly | Thr | Tyr | Lys | Val | Thr | Val | Ala | 35  | 40  | 45  |     |
| Val | Asp | Gln | Leu | Val | Glu | Glu | Gly | Thr | Asp | Gly | Tyr | Lys | Asp | Asp | Tyr | 50  | 55  | 60  |     |
| Thr | Phe | Thr | Val | Ala | Lys | Ser | Lys | Ala | Glu | Gln | Pro | Gly | Val | Tyr | Thr | 65  | 70  | 75  | 80  |
| Ser | Phe | Lys | Gln | Leu | Val | Thr | Ala | Met | Gln | Ser | Asn | Leu | Ser | Gly | Val | 85  | 90  | 95  |     |
| Tyr | Thr | Leu | Ala | Ser | Asp | Met | Thr | Ala | Asp | Glu | Val | Ser | Leu | Gly | Asp | 100 | 105 | 110 |     |
| Lys | Gln | Thr | Ser | Tyr | Leu | Thr | Gly | Ala | Phe | Thr | Gly | Ser | Leu | Ile | Gly | 115 | 120 | 125 |     |
| Ser | Asp | Gly | Thr | Lys | Ser | Tyr | Ala | Ile | Tyr | Asp | Leu | Lys | Lys | Pro | Leu | 130 | 135 | 140 |     |
| Phe | Asp | Thr | Leu | Asn | Gly | Ala | Thr | Val | Arg | Asp | Leu | Asp | Ile | Lys | Thr | 145 | 150 | 155 | 160 |
| Val | Ser | Ala | Asp | Ser | Lys | Glu | Asn | Val | Ala | Ala | Leu | Ala | Lys | Ala | Ala | 165 | 170 | 175 |     |
| Asn | Ser | Ala | Asn | Ile | Asn | Asn | Val | Ala | Val | Glu | Gly | Lys | Ile | Ser | Gly | 180 | 185 | 190 |     |
| Ala | Lys | Ser | Val | Ala | Gly | Leu | Val | Ala | Ser | Ala | Thr | Asn | Thr | Val | Ile | 195 | 200 | 205 |     |
| Glu | Asn | Ser | Ser | Phe | Thr | Gly | Lys | Leu | Ile | Ala | Asn | His | Gln | Asp | Ser | 210 | 215 | 220 |     |
| Asn | Lys | Asn | Asp | Thr | Gly | Gly | Ile | Val | Gly | Asn | Ile | Thr | Gly | Asn | Ser | 225 | 230 | 235 | 240 |
| Ser | Arg | Val | Asn | Lys | Val | Arg | Val | Asp | Ala | Leu | Ile | Ser | Thr | Asn | Ala | 245 | 250 | 255 |     |
| Arg | Asn | Asn | Asn | Gln | Thr | Ala | Gly | Gly | Ile | Val | Gly | Arg | Leu | Glu | Asn | 260 | 265 | 270 |     |
| Gly | Ala | Leu | Ile | Ser | Asn | Ser | Val | Ala | Thr | Gly | Glu | Ile | Arg | Asn | Gly | 275 | 280 | 285 |     |
| Gln | Gly | Tyr | Ser | Arg | Val | Gly | Gly | Ile | Val | Gly | Ser | Thr | Trp | Gln | Asn | 290 | 295 | 300 |     |
| Gly | Arg | Val | Asn | Asn | Val | Val | Ser | Asn | Val | Asp | Val | Gly | Asp | Gly | Tyr | 305 | 310 | 315 | 320 |

Val Ile Thr Gly Asp Gln Tyr Ala Ala Ala Asp Val Lys Asn Ala Ser  
325 330 335

Thr Ser Val Asp Asn Arg Lys Ala Asp Arg Phe Ala Thr Lys Leu Ser  
340 345 350

Lys Asp Gln Ile Asp Ala Lys Val Ala Asp Tyr Gly Ile Thr Val Thr  
355 360 365

Leu Asp Asp Thr Gly Gln Asp Leu Lys Arg Asn Leu Arg Glu Val Asp  
370 375 380

Tyr Thr Arg Leu Asn Lys Ala Glu Ala Glu Arg Lys Val Ala Tyr Ser  
385 390 395 400

Asn Ile Glu Lys Leu Met Pro Phe Tyr Asn Lys Asp Leu Val Val His  
405 410 415

Tyr Gly Asn Lys Val Ala Thr Thr Asp Lys Leu Tyr Thr Thr Glu Leu  
420 425 430

Leu Asp Val Val Pro Met Lys Asp Asp Glu Val Val Thr Asp Ile Asn  
435 440 445

Asn Lys Lys Asn Ser Ile Asn Lys Val Met Leu His Phe Lys Asp Asn  
450 455 460

Thr Val Glu Tyr Leu Asp Val Thr Phe Lys Glu Asn Phe Ile Asn Ser  
465 470 475 480

Gln Val Ile Glu Tyr Asn Val Thr Gly Lys Glu Tyr Ile Phe Thr Pro  
485 490 495

Glu Ala Phe Val Ser Asp Tyr Thr Ala Ile Thr Asn Asn Val Leu Ser  
500 505 510

Asp Leu Gln Asn Val Thr Leu Asn  
515 520

## (2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 850 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CTTTGGTTTT GAAGGAAGTA AGCGTGGACA ATTTGCTGTA GAAGGAATCA ATCAACTTCG | 60  |
| TGAGCATGTA GACACTCTAT TGATTATCTC AAACAACAAT TTGCTTGAAA TTGTTGATAA | 120 |
| GAAAACACCG CTTTTGGAGG CTCTTAGCGA AGCGGATAAC GTTCTTCGTC AAGGTGTTCA | 180 |
| AGGGATTACC GATTTGATTA CCAATCCAGG ATTGATTAAC CTTGACTTTG CCGATGTGAA | 240 |
| AACGGTAATG GCAAACAAAG GGAATGCTCT TATGGGTATT GGTATCGGTA GTGGAGAAGA | 300 |
| ACGTGTGGTA GAAGCGGCAC GTAAGGCAAT CTATTCACCA CTTCTTGAAA CAACTATTGA | 360 |
| CGGTGCTGAG GATGTTATCG TCAACGTTAC TGGTGGTCTT GACTTAACCT TGATTGAGGC | 420 |

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AGAAGAGGCT TCACAAATTG TGAACCAGGC AGCAGGTCAA GGAGTGAACA TCTGGCTCGG      480
TACTTCAATT GATGAAAGTA TGCGTGATGA AATTCGTGTA ACAGTTGTTG CAACGGGTGT      540
TCGTCAAGAC CGCGTAGAAA AGGTTGTGGC TCCACAAGCT AGATCTGCTA CTA ACTACCG      600
TGAGACAGTG AAACCAGCTC ATTCACATGG CTTTGATCGT CATTTTGATA TGGCAGAAAC      660
AGTTGAATTG CCAAAACAAA ATCCACGTCG TTTGGAACCA ACTCAGGCAT CTGCTTTTGG      720
TGATTGGGAT CTTGCGCGTG AATCGATTGT TCGTACAACA GATTCAGTCG TTTCTCCAGT      780
CGAGCGCTTT GAAGCCCCAA TTTCACAAGA TGAAGATGAA TTGGATACAC CTCCATTTTT      840
CAAAAATCGT                                     850

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(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 283 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

```

Phe Gly Phe Glu Gly Ser Lys Arg Gly Gln Phe Ala Val Glu Gly Ile
1          5          10
Asn Gln Leu Arg Glu His Val Asp Thr Leu Leu Ile Ile Ser Asn Asn
20        25        30
Asn Leu Leu Glu Ile Val Asp Lys Lys Thr Pro Leu Leu Glu Ala Leu
35        40        45
Ser Glu Ala Asp Asn Val Leu Arg Gln Gly Val Gln Gly Ile Thr Asp
50        55        60
Leu Ile Thr Asn Pro Gly Leu Ile Asn Leu Asp Phe Ala Asp Val Lys
65        70        75        80
Thr Val Met Ala Asn Lys Gly Asn Ala Leu Met Gly Ile Gly Ile Gly
85        90        95
Ser Gly Glu Glu Arg Val Val Glu Ala Ala Arg Lys Ala Ile Tyr Ser
100       105       110
Pro Leu Leu Glu Thr Thr Ile Asp Gly Ala Glu Asp Val Ile Val Asn
115       120       125
Val Thr Gly Gly Leu Asp Leu Thr Leu Ile Glu Ala Glu Glu Ala Ser
130       135       140
Gln Ile Val Asn Gln Ala Ala Gly Gln Gly Val Asn Ile Trp Leu Gly
145       150       155       160
Thr Ser Ile Asp Glu Ser Met Arg Asp Glu Ile Arg Val Thr Val Val
165       170       175
Ala Thr Gly Val Arg Gln Asp Arg Val Glu Lys Val Val Ala Pro Gln

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 180 |     | 185 |     | 190 |     |     |     |     |     |     |     |     |     |     |
| Ala | Arg | Ser | Ala | Thr | Asn | Tyr | Arg | Glu | Thr | Val | Lys | Pro | Ala | His | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Gly | Phe | Asp | Arg | His | Phe | Asp | Met | Ala | Glu | Thr | Val | Glu | Leu | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Gln | Asn | Pro | Arg | Arg | Leu | Glu | Pro | Thr | Gln | Ala | Ser | Ala | Phe | Gly |
|     | 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |
| Asp | Trp | Asp | Leu | Arg | Arg | Glu | Ser | Ile | Val | Arg | Thr | Thr | Asp | Ser | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Ser | Pro | Val | Glu | Arg | Phe | Glu | Ala | Pro | Ile | Ser | Gln | Asp | Glu | Asp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Leu | Asp | Thr | Pro | Pro | Phe | Phe | Lys | Asn | Arg |     |     |     |     |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1051 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| CTACTACCTC  | TCGAGAGAAA | GTGACCTAGA  | GGTGACCGTT | TTTGACCATG | AGCAAGGTCA | 60  |
| AGCCACCAAG  | GCCGCAGCAG | GAATTATCAG  | TCCTTGTTT  | TCCAAACGCC | GTAATAAAGC | 120 |
| CTGGTACAAG  | ATGGCGCGCT | TGGGGGCTGA  | TTTTTATGTG | GATTTATTAG | CTGATTTAGA | 180 |
| GAAATCAGGA  | CAAGAAATCG | ACTTTTACCA  | GCGTTCGGGA | GTCTTTCTCT | TGAAAAAGGA | 240 |
| TGAATCCAAT  | TTGGAAGAAC | TTTATCAACT  | GGCCCTCCAG | CGCAGAGAAG | AATCTCCCTT | 300 |
| GATAGGGCAA  | TTAGCCATTC | TGAACCAAGC  | CTCAGCTAAT | GAATTATTC  | CTGGTTTGCA | 360 |
| GGGATTTGAC  | CGCCTGCTCT | ATGCTTCTGG  | TGGAGCGAGA | GATAGTGGCC | AACTTTTAGT | 420 |
| GACTCGTTTG  | CTGGAAGTCA | GTCATGTCAA  | GCTGGTCAAA | GAAAAAGTGA | CTCTGACACC | 480 |
| GTTAGCATCA  | GGCTACCAGA | TTGGTGAAGA  | GGAGTTTGAG | CAGGTTATTT | TGGCGACGGG | 540 |
| AGCTTGTTTG  | GGGGACATGT | TAGAGCCTTT  | AGGTTATGAA | GTGGATGTCC | GTCCTCAAAA | 600 |
| AGGACAACCTA | CGAGATTATC | AGCTTGCCCA  | AGACATGGAA | GATTACCCTG | TTGTCATGCC | 660 |
| AGAAGGGGAG  | TGGGATTTGA | TTCCCTTTGC  | AGGTGGGAAA | TTATCCTTAG | GCGCTACCCA | 720 |
| CGAAAATGAC  | ATGGGATTTG | ATTTGACGGT  | AGATGAAACC | TTGCTCCAAC | AAATGGAGGA | 780 |
| GGCCACCTTG  | ACTCACTATC | TGATTTTGGC  | TGAAGCTACT | TCAAAATCTG | AGCGTGTG   | 840 |
| AATCCGTGCC  | TACACCAGTG | ATTTCTCTCC  | TTTCTTTGGG | CAGGTGCCTG | ACTTAACTGG | 900 |
| TGTCTATGCA  | GCCAGTGGAC | TAGGTTTCATC | AGGCCTCACA | ACTGGTCCTA | TCATTGGTTA | 960 |

CCATCTAGCC CAACTGATCC AAGACAAGGA GTTGACCTTG GACCCTCTAA ATTACCCAAT 1020  
 TGAAAACCTAT GTCAAACGAG TAAAAAGCGA A 1051

## (2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 350 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Tyr Tyr Leu Ser Arg Glu Ser Asp Leu Glu Val Thr Val Phe Asp His  
 1 5 10 15  
 Glu Gln Gly Gln Ala Thr Lys Ala Ala Ala Gly Ile Ile Ser Pro Trp  
 20 25 30  
 Phe Ser Lys Arg Arg Asn Lys Ala Trp Tyr Lys Met Ala Arg Leu Gly  
 35 40 45  
 Ala Asp Phe Tyr Val Asp Leu Leu Ala Asp Leu Glu Lys Ser Gly Gln  
 50 55 60  
 Glu Ile Asp Phe Tyr Gln Arg Ser Gly Val Phe Leu Leu Lys Lys Asp  
 65 70 75 80  
 Glu Ser Asn Leu Glu Glu Leu Tyr Gln Leu Ala Leu Gln Arg Arg Glu  
 85 90 95  
 Glu Ser Pro Leu Ile Gly Gln Leu Ala Ile Leu Asn Gln Ala Ser Ala  
 100 105 110  
 Asn Glu Leu Phe Pro Gly Leu Gln Gly Phe Asp Arg Leu Leu Tyr Ala  
 115 120 125  
 Ser Gly Gly Ala Arg Val Asp Gly Gln Leu Leu Val Thr Arg Leu Leu  
 130 135 140  
 Glu Val Ser His Val Lys Leu Val Lys Glu Lys Val Thr Leu Thr Pro  
 145 150 155 160  
 Leu Ala Ser Gly Tyr Gln Ile Gly Glu Glu Glu Phe Glu Gln Val Ile  
 165 170 175  
 Leu Ala Thr Gly Ala Trp Leu Gly Asp Met Leu Glu Pro Leu Gly Tyr  
 180 185 190  
 Glu Val Asp Val Arg Pro Gln Lys Gly Gln Leu Arg Asp Tyr Gln Leu  
 195 200 205  
 Ala Gln Asp Met Glu Asp Tyr Pro Val Val Met Pro Glu Gly Glu Trp  
 210 215 220  
 Asp Leu Ile Pro Phe Ala Gly Gly Lys Leu Ser Leu Gly Ala Thr His  
 225 230 235 240  
 Glu Asn Asp Met Gly Phe Asp Leu Thr Val Asp Glu Thr Leu Leu Gln  
 245 250 255

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Met | Glu | Glu | Ala | Thr | Leu | Thr | His | Tyr | Leu | Ile | Leu | Ala | Glu | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Ser | Lys | Ser | Glu | Arg | Val | Gly | Ile | Arg | Ala | Tyr | Thr | Ser | Asp | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ser | Pro | Phe | Phe | Gly | Gln | Val | Pro | Asp | Leu | Thr | Gly | Val | Tyr | Ala | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ser | Gly | Leu | Gly | Ser | Ser | Gly | Leu | Thr | Thr | Gly | Pro | Ile | Ile | Gly | Tyr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| His | Leu | Ala | Gln | Leu | Ile | Gln | Asp | Lys | Glu | Leu | Thr | Leu | Asp | Pro | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asn | Tyr | Pro | Ile | Glu | Asn | Tyr | Val | Lys | Arg | Val | Lys | Ser | Glu |     |     |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TAAGGTCAA  | AGTCAGACCG | CTAAGAAAGT | GCTAGAAAAG | ATTGGAGCTG | ACTCGGTTAT | 60  |
| CTCGCCAGAG | TATGAAATGG | GGCAGTCTCT | AGCACAGACC | ATTCTTTTCC | ATAATAGTGT | 120 |
| TGATGTCTTT | CAGTTGGATA | AAAATGTGTC | TATCGTGGAG | ATGAAAATTC | CTCAGTCTTG | 180 |
| GGCAGGTCAA | AGTCTGAGTA | AATTAGACCT | CCGTGGCAAA | TACAATCTGA | ATATTTTGGG | 240 |
| TTTCCGAGAG | CAGGAAAATT | CCCCATTGGA | TGTTGAATTT | GGACCAGATG | ACCTCTTGAA | 300 |
| AGCAGATACC | TATATTTTGG | CAGTCATCAA | CAACCAGTAT | TTGGATACCC | TA         | 352 |

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Lys | Ser | Gln | Thr | Ala | Lys | Lys | Val | Leu | Glu | Lys | Ile | Gly | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Ser | Val | Ile | Ser | Pro | Glu | Tyr | Glu | Met | Gly | Gln | Ser | Leu | Ala | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ile | Leu | Phe | His | Asn | Ser | Val | Asp | Val | Phe | Gln | Leu | Asp | Lys | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Val Ser Ile Val Glu Met Lys Ile Pro Gln Ser Trp Ala Gly Gln Ser  
 50 55 60

Leu Ser Lys Leu Asp Leu Arg Gly Lys Tyr Asn Leu Asn Ile Leu Gly  
 65 70 75 80

Phe Arg Glu Gln Glu Asn Ser Pro Leu Asp Val Glu Phe Gly Pro Asp  
 85 90 95

Asp Leu Leu Lys Ala Asp Thr Tyr Ile Leu Ala Val Ile Asn Asn Gln  
 100 105 110

Tyr Leu Asp Thr Leu  
 115

## (2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 247 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

TGACGGGTCT CAGGATCAGA CTCAGGAAAT CGCTGAGTGT TTAGCTAGCA AGTATCCTAA 60  
 TATCGTTAGA GCCATCTATC AGGAAAATAA ATGCCATGGC GGTGCGGTCA ATCGTGGCTT 120  
 GGTAGAGGCT TCTGGGCGCT ATTTTAAAGT AGTTGACAGT GATGACTGGG TGGATCCTCG 180  
 TGCCTACTTG AAAATTCTTG AACTTGCAG GAACTTGAGA GCAAAGGTCA AGAGGTGGAT 240  
 GTCTTTG 247

## (2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 82 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Gly Ser Gln Asp Gln Thr Gln Glu Ile Ala Glu Cys Leu Ala Ser  
 1 5 10 15

Lys Tyr Pro Asn Ile Val Arg Ala Ile Tyr Gln Glu Asn Lys Cys His  
 20 25 30

Gly Gly Ala Val Asn Arg Gly Leu Val Glu Ala Ser Gly Arg Tyr Phe  
 35 40 45

Lys Val Val Asp Ser Asp Asp Trp Val Asp Pro Arg Ala Tyr Leu Lys  
 50 55 60

Ile Leu Glu Thr Cys Arg Asn Leu Arg Ala Lys Val Lys Arg Trp Met

65

70

75

80

Ser Leu

## (2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1744 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TAGAGGCTTT GCCAAATGGT GGAAGGGCA CGAGCGTCGA AAAGAGGAAC GCTTTGTCAA   | 60   |
| ACAAGAAGAA AAAGCTCGCC AAAAGGCTGA GAAAGAGGCT AGATTAGAAC AAGAAGAGAC  | 120  |
| TGAAAAAGCC TTACTCGATT TGCCTCCTGT TGATATGGAA ACGGGTGAAA TTCTGACAGA  | 180  |
| GGAAGCTGTT CAAAATCTTC CACCTATTCC AGAAGAAAAG TGGGTGGAAC CAGAAATCAT  | 240  |
| CCTGCCTCAA GCTGAACTTA AATTCCCTGA ACAGGAAGAT GACTCAGATG ACGAAGATGT  | 300  |
| TCAGGTCGAT TTTTCAGCCA AAGAAGCCCT TGAATACAAA CTTCCAAGCT TACAACTCTT  | 360  |
| TGCACCAGAT AAACCAAAAG ATCAGTCTAA AGAGAAGAAA ATTGTCAGAG AAAATATCAA  | 420  |
| AATCTTAGAA GCAACCTTTG CTAGCTTTGG TATTAAGGTA ACAGTTGAAC GGGCCGAAAT  | 480  |
| TGGGCCATCA GTGACCAAGT ATGAAGTCAA GCCGGCTGTT GGTGTAAGGG TCAACCGCAT  | 540  |
| TTCCAATCTA TCAGATGACC TCGCTCTAGC CTTGGCTGCC AAAGATGTCC GGATTGAAGC  | 600  |
| ACCAATCCCT GGGAAATCCC TAATCGGAAT TGAAGTGCCC AACTCCGATA TTGCCACTGT  | 660  |
| ATCTTTCCGA GAACTATGGG AACAAATCGCA AACGAAAGCA GAAAATTTCT TGGAAATTC  | 720  |
| TTTAGGGAAG GCTGTTAATG GAACCGCAAG AGCTTTTGAC CTTTCTAAAA TGCCCCACTT  | 780  |
| GCTAGTTGCA GGTTCACGG GTTCAGGGAA GTCAGTAGCA GTTAACGGCA TTATTGCTAG   | 840  |
| CATTCTCATG AAGGCGAGAC CAGATCAAGT TAAATTTATG ATGGTCGATC CCAAGATGGT  | 900  |
| TGAGTTATCT GTTTACAATG ATATTCCCCA CCTCTTGATT CCAGTCGTGA CCAATCCACG  | 960  |
| CAAAGCCAGC AAGGCTCTGC AAAAGGTTGT GGATGAAATG GAAAACCGTT ATGAACTCTT  | 1020 |
| TGCCAAGGTG GGAGTTCGGA ATATTGCAGG TTTTAATGCC AAGGTAGAAG AGTTCAATTC  | 1080 |
| CCAGTCTGAG TACAAGCAAA TTCCGCTACC ATTCAATTGTC GTGATTGTGG ATGAGTTGGC | 1140 |
| TGACCTCATG ATGGTGGCCA GCAAGGAAGT GGAAGATGCT ATCATCCGTC TTGGGCAGAA  | 1200 |
| GGCGCGTGCT GCAGGTATCC ACATGATTCT TGCAACTCAG CGTCCATCTG TTGATGTCAT  | 1260 |
| CTCTGGTTTG ATTAAGGCCA ATGTTCCATC TCGTGTAGCA TTTGCGGTTT CATCAGGAAC  | 1320 |
| AGACTCCCGT ACGATTTTGG ATGAAAATGG AGCAGAAAAA CTTCTTGGTC GAGGAGACAT  | 1380 |
| GCTCTTTAAA CCGATTGATG AAAATCATCC AGTTCGTCTC CAAGGCTCCT TTATCTCGGA  | 1440 |

TGACGATGTT GAGCGCATTG TGAAC TTCAT CAAGACTCAG GCAGATGCAG ACTACGATGA 1500  
 GAGTTTTGAT CCAGGTGAGG TTTCTGAAAA TGAAGGAGAA TTTTCGGATG GAGATGCTGG 1560  
 TGGTGATCCG CTTTTTGAAG AAGCTAAGTC TTTGGTTATC GAAACACAGA AAGCCAGTGC 1620  
 GTCTATGATT CAGCGTCGTT TATCAGTTGG ATTTAACCGT GCGACCCGTC TCATGGAAGA 1680  
 ACTGGAGATA GCAGGTGTCA TCGGTCCAGC TGAAGGTACC AAACCTCGAA AAGTGTTACA 1740  
 ACAA 1744

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 581 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Arg Gly Phe Ala Lys Trp Trp Glu Gly His Glu Arg Arg Lys Glu Glu  
 1 5 10 15  
 Arg Phe Val Lys Gln Glu Glu Lys Ala Arg Gln Lys Ala Glu Lys Glu  
 20 25 30  
 Ala Arg Leu Glu Gln Glu Glu Thr Glu Lys Ala Leu Leu Asp Leu Pro  
 35 40 45  
 Pro Val Asp Met Glu Thr Gly Glu Ile Leu Thr Glu Glu Ala Val Gln  
 50 55 60  
 Asn Leu Pro Pro Ile Pro Glu Glu Lys Trp Val Glu Pro Glu Ile Ile  
 65 70 75 80  
 Leu Pro Gln Ala Glu Leu Lys Phe Pro Glu Gln Glu Asp Asp Ser Asp  
 85 90 95  
 Asp Glu Asp Val Gln Val Asp Phe Ser Ala Lys Glu Ala Leu Glu Tyr  
 100 105 110  
 Lys Leu Pro Ser Leu Gln Leu Phe Ala Pro Asp Lys Pro Lys Asp Gln  
 115 120 125  
 Ser Lys Glu Lys Lys Ile Val Arg Glu Asn Ile Lys Ile Leu Glu Ala  
 130 135 140  
 Thr Phe Ala Ser Phe Gly Ile Lys Val Thr Val Glu Arg Ala Glu Ile  
 145 150 155 160  
 Gly Pro Ser Val Thr Lys Tyr Glu Val Lys Pro Ala Val Gly Val Arg  
 165 170 175  
 Val Asn Arg Ile Ser Asn Leu Ser Asp Asp Leu Ala Leu Ala Leu Ala  
 180 185 190  
 Ala Lys Asp Val Arg Ile Glu Ala Pro Ile Pro Gly Lys Ser Leu Ile  
 195 200 205

Gly Ile Glu Val Pro Asn Ser Asp Ile Ala Thr Val Ser Phe Arg Glu  
 210 215 220  
 Leu Trp Glu Gln Ser Gln Thr Lys Ala Glu Asn Phe Leu Glu Ile Pro  
 225 230 235 240  
 Leu Gly Lys Ala Val Asn Gly Thr Ala Arg Ala Phe Asp Leu Ser Lys  
 245 250 255  
 Met Pro His Leu Leu Val Ala Gly Ser Thr Gly Ser Gly Lys Ser Val  
 260 265 270  
 Ala Val Asn Gly Ile Ile Ala Ser Ile Leu Met Lys Ala Arg Pro Asp  
 275 280 285  
 Gln Val Lys Phe Met Met Val Asp Pro Lys Met Val Glu Leu Ser Val  
 290 295 300  
 Tyr Asn Asp Ile Pro His Leu Leu Ile Pro Val Val Thr Asn Pro Arg  
 305 310 315 320  
 Lys Ala Ser Lys Ala Leu Gln Lys Val Val Asp Glu Met Glu Asn Arg  
 325 330 335  
 Tyr Glu Leu Phe Ala Lys Val Gly Val Arg Asn Ile Ala Gly Phe Asn  
 340 345 350  
 Ala Lys Val Glu Glu Phe Asn Ser Gln Ser Glu Tyr Lys Gln Ile Pro  
 355 360 365  
 Leu Pro Phe Ile Val Val Ile Val Asp Glu Leu Ala Asp Leu Met Met  
 370 375 380  
 Val Ala Ser Lys Glu Val Glu Asp Ala Ile Ile Arg Leu Gly Gln Lys  
 385 390 395 400  
 Ala Arg Ala Ala Gly Ile His Met Ile Leu Ala Thr Gln Arg Pro Ser  
 405 410 415  
 Val Asp Val Ile Ser Gly Leu Ile Lys Ala Asn Val Pro Ser Arg Val  
 420 425 430  
 Ala Phe Ala Val Ser Ser Gly Thr Asp Ser Arg Thr Ile Leu Asp Glu  
 435 440 445  
 Asn Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp Met Leu Phe Lys Pro  
 450 455 460  
 Ile Asp Glu Asn His Pro Val Arg Leu Gln Gly Ser Phe Ile Ser Asp  
 465 470 475 480  
 Asp Asp Val Glu Arg Ile Val Asn Phe Ile Lys Thr Gln Ala Asp Ala  
 485 490 495  
 Asp Tyr Asp Glu Ser Phe Asp Pro Gly Glu Val Ser Glu Asn Glu Gly  
 500 505 510  
 Glu Phe Ser Asp Gly Asp Ala Gly Gly Asp Pro Leu Phe Glu Glu Ala  
 515 520 525  
 Lys Ser Leu Val Ile Glu Thr Gln Lys Ala Ser Ala Ser Met Ile Gln  
 530 535 540

Arg Arg Leu Ser Val Gly Phe Asn Arg Ala Thr Arg Leu Met Glu Glu  
 545 550 555 560  
 Leu Glu Ile Ala Gly Val Ile Gly Pro Ala Glu Gly Thr Lys Pro Arg  
 565 570 575  
 Lys Val Leu Gln Gln  
 580

## (2) INFORMATION FOR SEQ ID NO: 133:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 829 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TCAAAAAGAG AAGGAAAAC TGGTTATTGC TGGGAAAATA GGTCCAGAAC CAGAAATTTT   | 60  |
| GGCCAATATG TATAAGTTGC TGATTGAAGA AAATACCAGC ATGACTGCGA CTGTTAAACC  | 120 |
| GAATTTTGGG AAGACAAGCT TCCTTTATGA AGCTCTGAAA AAAGGCGATA TTGACATCTA  | 180 |
| TCCTGAATTT ACTGGTACGG TGA CTGAAAG TTTGCTTCAA CCATCACCCA AGGTGAGTCA | 240 |
| TGAACCAGAA CAGGTTTATC AGGTGGCGCG TGATGGCATT GCTAAGCAGG ATCATCTAGC  | 300 |
| CTATCTCAAA CCCATGTCTT ATCAAAACAC CTATGCTGTA GCTGTTCCGA AAAAGATTGC  | 360 |
| TCAAGAATAT GGCTTGAAGA CCATTTTACA CTTGAAAAAA GTGGAAGGGC AGTTGAAGGC  | 420 |
| AGGTTTTACA CTCGAGTTTA ACGACCGTGA AGATGGAAAT AAGGGCTTGC AATCAATGTA  | 480 |
| TGGTCTCAAT CTCAATGTAG CGACCATTGA GCCAGCCCTT CGCTATCAGG CTATTTCAGTC | 540 |
| AGGGGATATT CAAATCACGG ATGCCTATTC GACTGATGCG GAATTGGAGC GTTATGATTT  | 600 |
| ACAGGTCTTG GAAGATGACA AGCAACTCTT CCCACCTTAT CAAGGGGCTC CACTCATGAA  | 660 |
| AGAAGCTCTT CTCAAGAAAC ACCCAGAGTT GGAAAGAGTT CTTAATACAT TGGCTGGTAA  | 720 |
| GATTACAGAA AGCCAGATGA GCCAGCTCAA CTACCAAGTC GGTGTTGAAG GCAAGTCAGC  | 780 |
| AAAGCAAGTA GCCAAGGAGT TTCTCCAAGA ACAAGGTTTG TTGAAGAAA              | 829 |

## (2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 276 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

|                                                                 |
|-----------------------------------------------------------------|
| Gln Lys Glu Lys Glu Asn Leu Val Ile Ala Gly Lys Ile Gly Pro Glu |
| 1 5 10 15                                                       |

Pro Glu Ile Leu Ala Asn Met Tyr Lys Leu Leu Ile Glu Glu Asn Thr  
                   20                                  25                                  30  
 Ser Met Thr Ala Thr Val Lys Pro Asn Phe Gly Lys Thr Ser Phe Leu  
                   35                                  40                                  45  
 Tyr Glu Ala Leu Lys Lys Gly Asp Ile Asp Ile Tyr Pro Glu Phe Thr  
                   50                                  55                                  60  
 Gly Thr Val Thr Glu Ser Leu Leu Gln Pro Ser Pro Lys Val Ser His  
                   65                                  70                                  75                                  80  
 Glu Pro Glu Gln Val Tyr Gln Val Ala Arg Asp Gly Ile Ala Lys Gln  
                                   85                                  90                                  95  
 Asp His Leu Ala Tyr Leu Lys Pro Met Ser Tyr Gln Asn Thr Tyr Ala  
                                   100                                  105                                  110  
 Val Ala Val Pro Lys Lys Ile Ala Gln Glu Tyr Gly Leu Lys Thr Ile  
                                   115                                  120                                  125  
 Ser Asp Leu Lys Lys Val Glu Gly Gln Leu Lys Ala Gly Phe Thr Leu  
                   130                                  135                                  140  
 Glu Phe Asn Asp Arg Glu Asp Gly Asn Lys Gly Leu Gln Ser Met Tyr  
                   145                                  150                                  155                                  160  
 Gly Leu Asn Leu Asn Val Ala Thr Ile Glu Pro Ala Leu Arg Tyr Gln  
                                   165                                  170                                  175  
 Ala Ile Gln Ser Gly Asp Ile Gln Ile Thr Asp Ala Tyr Ser Thr Asp  
                                   180                                  185                                  190  
 Ala Glu Leu Glu Arg Tyr Asp Leu Gln Val Leu Glu Asp Asp Lys Gln  
                                   195                                  200                                  205  
 Leu Phe Pro Pro Tyr Gln Gly Ala Pro Leu Met Lys Glu Ala Leu Leu  
                   210                                  215                                  220  
 Lys Lys His Pro Glu Leu Glu Arg Val Leu Asn Thr Leu Ala Gly Lys  
                   225                                  230                                  235                                  240  
 Ile Thr Glu Ser Gln Met Ser Gln Leu Asn Tyr Gln Val Gly Val Glu  
                                   245                                  250                                  255  
 Gly Lys Ser Ala Lys Gln Val Ala Lys Glu Phe Leu Gln Glu Gln Gly  
                                   260                                  265                                  270  
 Leu Leu Lys Lys  
                                   275

## (2) INFORMATION FOR SEQ ID NO: 135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 712 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

```

ACGTTCTATT GAGGACCACT TTGATTCAAA CTTCGAATTG GAATATAACC TCAAAGAAAA      60
AGGGAAAACA GATCTTTTGA AGCTAGTTGA TAAACAACCT GACATGCGTC TGCATTTTAT      120
CCGCCAAACT CATCCACGCG GTCTCGGAGA TGCTGTTTTG CAAGCCAAGG CTTTCGTCGG      180
AAATGAACCT TTTGTCTGTTA TGCTTGTTGA TGACTTGATG GATATCACAG ACGAAAAGGC      240
TGTTCCACTT ACCAAACAAC TCATGGATGA CTACGAGCGT ACCCAGCGCT CTACTATCGC      300
TGTCATGCCA GTCCCTCATG ACGAAGTATC TGCTTACGGG GTTATTGCTC CGCAAGGCCA      360
AGGAAAAGAT GGTCTTTACA GTGTTGAAAC CTTTGTGTA AAACCAGCTC CAGAGGACGC      420
TCCTAGCGAC CTTGCTATTA TCGGACGCTA CCTCCTCACG CCTGAAATTT TTGAGATTCT      480
CGAAAAGCAA GCTCCAGGTG CAGGAAATGA AATTCAGCTG ACAGATGCAA TCGACACCCT      540
CAATAAAACA CAACGTGTAT TTGCTCGTGA GTTCAAAGGG GCTCGTTACG ATGTCGGAGA      600
CAAGTTTGGC TTCATGAAAA CATCCATCGA CTACGCCCTC AAACACCCAC AAGTCAAAGA      660
TGATTTGAAG AATTACCTCA TCCAACCTGG AAAAGAATTG ACTGAGAAGG AA              712

```

## (2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 237 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```

Arg Ser Ile Glu Asp His Phe Asp Ser Asn Phe Glu Leu Glu Tyr Asn
1          5          10          15
Leu Lys Glu Lys Gly Lys Thr Asp Leu Leu Lys Leu Val Asp Lys Thr
20          25          30
Thr Asp Met Arg Leu His Phe Ile Arg Gln Thr His Pro Arg Gly Leu
35          40          45
Gly Asp Ala Val Leu Gln Ala Lys Ala Phe Val Gly Asn Glu Pro Phe
50          55          60
Val Val Met Leu Gly Asp Asp Leu Met Asp Ile Thr Asp Glu Lys Ala
65          70          75          80
Val Pro Leu Thr Lys Gln Leu Met Asp Asp Tyr Glu Arg Thr His Ala
85          90          95
Ser Thr Ile Ala Val Met Pro Val Pro His Asp Glu Val Ser Ala Tyr
100         105         110
Gly Val Ile Ala Pro Gln Gly Glu Gly Lys Asp Gly Leu Tyr Ser Val
115         120         125
Glu Thr Phe Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Asp Leu
130         135         140

```

Ala Ile Ile Gly Arg Tyr Leu Leu Thr Pro Glu Ile Phe Glu Ile Leu  
 145 150 155 160  
 Glu Lys Gln Ala Pro Gly Ala Gly Asn Glu Ile Gln Leu Thr Asp Ala  
 165 170 175  
 Ile Asp Thr Leu Asn Lys Thr Gln Arg Val Phe Ala Arg Glu Phe Lys  
 180 185 190  
 Gly Ala Arg Tyr Asp Val Gly Asp Lys Phe Gly Phe Met Lys Thr Ser  
 195 200 205  
 Ile Asp Tyr Ala Leu Lys His Pro Gln Val Lys Asp Asp Leu Lys Asn  
 210 215 220  
 Tyr Leu Ile Gln Leu Gly Lys Glu Leu Thr Glu Lys Glu  
 225 230 235

## (2) INFORMATION FOR SEQ ID NO: 137:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 502 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CGCTCAAAAT ACCAGAGGTG TTCAGCTAAT CGAGCACGTT TCTCCTCAAA TGTTGAAAGC | 60  |
| CCAATTGGAG AGTGTCTTTT CTGATATTCC ACCTCAGGCT GTAAAACTG GAATGTTGGC  | 120 |
| TACTACTGAA ATCATGGAAA TCATCCAACC CTATCTTAAA AAAGTGGATT GTCCCTATGT | 180 |
| CCTTGATCCT GTTATGGTTG CTACAAGTGG AGATGCCTTG ATTGACTCAA ATGCTAGAGA | 240 |
| CTATCTCAAA ACAAACTTAC TACCTCTAGC AACTATTATT ACGCCAAATC TTCCTGAAGC | 300 |
| AGAAGAGATT GTTGGTTTTT CAATCCATGA CCCCAGAGAC ATGCAGCGTG CTGGTCGCCT | 360 |
| GATTTTAAAA GAATTTGGTC CTCAGTCTGT GGTTATCAAA GGCGGACATC TCAAAGGTGG | 420 |
| TGCTAAAGAT TTCCTCTTTA CCAAGAATGA ACAATTTGTC TGGGAAAGCC CACGAATTCA | 480 |
| AACCTGTCAC ACCCATGGTA CT                                          | 502 |

## (2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 167 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Asn | Thr | Arg | Gly | Val | Gln | Leu | Ile | Glu | His | Val | Ser | Pro | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Met Leu Lys Ala Gln Leu Glu Ser Val Phe Ser Asp Ile Pro Pro Gln  
20 25 30  
Ala Val Lys Thr Gly Met Leu Ala Thr Thr Glu Ile Met Glu Ile Ile  
35 40 45  
Gln Pro Tyr Leu Lys Lys Leu Asp Cys Pro Tyr Val Leu Asp Pro Val  
50 55 60  
Met Val Ala Thr Ser Gly Asp Ala Leu Ile Asp Ser Asn Ala Arg Asp  
65 70 75 80  
Tyr Leu Lys Thr Asn Leu Leu Pro Leu Ala Thr Ile Ile Thr Pro Asn  
85 90 95  
Leu Pro Glu Ala Glu Glu Ile Val Gly Phe Ser Ile His Asp Pro Glu  
100 105 110  
Asp Met Gln Arg Ala Gly Arg Leu Ile Leu Lys Glu Phe Gly Pro Gln  
115 120 125  
Ser Val Val Ile Lys Gly Gly His Leu Lys Gly Gly Ala Lys Asp Phe  
130 135 140  
Leu Phe Thr Lys Asn Glu Gln Phe Val Trp Glu Ser Pro Arg Ile Gln  
145 150 155 160  
Thr Cys His Thr His Gly Thr  
165

## (2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 805 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AATTGTACAA TTAGAAAAAG ATAGCAAATC AGACAAAGAA CAAGTTGATA AACTATTTGA | 60  |
| ATCATTTGAT GCATCTTCAG ATGAATCTAT TTCTAAATTA AAAGAACTAT CTGAACTTC  | 120 |
| ACTTAAACC GATGCAGGTA AAGACTATCT TAATAACAAA GTCAAAGAAT CATCTAAAGC  | 180 |
| AATTGTAGAT TTTCATTTGC AAAAAGGTTT GGCTTATGAT GTTAAAGATT CAGATGACAA | 240 |
| ATTTAAAGAT AAAGCACTC TTGAAACAAA TGTAAGAA ATTACAAAAC AAATTGATTT    | 300 |
| TATCAAAAAA GTTGATGAAA CTTTTAAACA AGAGAATTTG GAAGAACTC TTAAATCTCT  | 360 |
| AAATGATCTT GTTGATAAAT ATCAAAAACA AATCGAACTT TTGAAGAAAG AAGAAGAAAA | 420 |
| AGCTGCTGAA AAAGCTGCTG AAAAAGCAAA GGAATCTTCT AGTCAAAGTA ATTCTTCTGG | 480 |
| TAGTGCTTCT AATGAGTCTT ATAATGGATC TTCCAATTCA AATGTAGATT ATAGTTCATC | 540 |
| TGAACAAACT AATGGATATT CAAATAATTA TGGCGGTCAA GATTATTCTG GTTCAGGAGA | 600 |
| TAGTTCAACA AATGGTGGAT CATCAGAACA ATATTCATCT AGCAATTCAA ACAGCGGAGC | 660 |

AAATAATGTC TACAGATATA AAGGCACTGG TGCTGACGGC TATCAAAGAT ACTACTACAA 720  
 AGATCATAAT AATGGAGATG TGTATGATGA CGATGGAAAT TACCTTGGA ACTTTGGTGG 780  
 CGGCATTGCA GAACCTAGTC AACGC 805

## (2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 268 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ile Val Gln Leu Glu Lys Asp Ser Lys Ser Asp Lys Glu Gln Val Asp  
 1 5 10 15  
 Lys Leu Phe Glu Ser Phe Asp Ala Ser Ser Asp Glu Ser Ile Ser Lys  
 20 25 30  
 Leu Lys Glu Leu Ser Glu Thr Ser Leu Lys Thr Asp Ala Gly Lys Asp  
 35 40 45  
 Tyr Leu Asn Asn Lys Val Lys Glu Ser Ser Lys Ala Ile Val Asp Phe  
 50 55 60  
 His Leu Gln Lys Gly Leu Ala Tyr Asp Val Lys Asp Ser Asp Asp Lys  
 65 70 75 80  
 Phe Lys Asp Lys Ala Thr Leu Glu Thr Asn Val Lys Glu Ile Thr Lys  
 85 90 95  
 Gln Ile Asp Phe Ile Lys Lys Val Asp Glu Thr Phe Lys Gln Glu Asn  
 100 105 110  
 Leu Glu Glu Thr Leu Lys Ser Leu Asn Asp Leu Val Asp Lys Tyr Gln  
 115 120 125  
 Lys Gln Ile Glu Leu Leu Lys Lys Glu Glu Glu Lys Ala Ala Glu Lys  
 130 135 140  
 Ala Ala Glu Lys Ala Lys Glu Ser Ser Ser Gln Ser Asn Ser Ser Gly  
 145 150 155 160  
 Ser Ala Ser Asn Glu Ser Tyr Asn Gly Ser Ser Asn Ser Asn Val Asp  
 165 170 175  
 Tyr Ser Ser Ser Glu Gln Thr Asn Gly Tyr Ser Asn Asn Tyr Gly Gly  
 180 185 190  
 Gln Asp Tyr Ser Gly Ser Gly Asp Ser Ser Thr Asn Gly Gly Ser Ser  
 195 200 205  
 Glu Gln Tyr Ser Ser Ser Asn Ser Asn Ser Gly Ala Asn Asn Val Tyr  
 210 215 220  
 Arg Tyr Lys Gly Thr Gly Ala Asp Gly Tyr Gln Arg Tyr Tyr Tyr Lys  
 225 230 235 240

Asp His Asn Asn Gly Asp Val Tyr Asp Asp Asp Gly Asn Tyr Leu Gly  
                   245                  250                  255

Asn Phe Gly Gly Gly Ile Ala Glu Pro Ser Gln Arg  
                   260                  265

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 211 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TCTGACCAAG CAAAAGAAG CAGTCAATGA CAAAGGAAAA GCAGCTGTTG TTAAGGTGGT  | 60  |
| GGAAAGCCAG GCAGAACTTT ATAGCTTAGA AAAGAATGAA GATGCTAGCC TAAGAAAGTT | 120 |
| ACAAGCAGAT GGACGCATCA CGGAAGAACA GGCTAAAGCT TATAAAGAAT ACAATGATAA | 180 |
| AAATGGAGGA GCAAATCGTA AAGTCAATGA T                                | 211 |

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Leu Thr Lys Gln Lys Glu Ala Val Asn Asp Lys Gly Lys Ala Ala Val | 15 |
| 1                  5                  10                        |    |
| Val Lys Val Val Glu Ser Gln Ala Glu Leu Tyr Ser Leu Glu Lys Asn | 30 |
| 20                  25                                          |    |
| Glu Asp Ala Ser Leu Arg Lys Leu Gln Ala Asp Gly Arg Ile Thr Glu | 45 |
| 35                  40                                          |    |
| Glu Gln Ala Lys Ala Tyr Lys Glu Tyr Asn Asp Lys Asn Gly Gly Ala | 60 |
| 50                  55                  60                      |    |
| Asn Arg Lys Val Asn Asp                                         | 70 |
| 65                  70                                          |    |

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

```

GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC GGTAGAGGAA CAGATTTTCT TTATGGAGTT      60
TGAAGAACTC TATCGGGAAA CCCAAAAACG CAGTGTAGCC AGTCAGCAAA AGACTAGTCT      120
GAACTTAGAT GGGCAGACGC TTAGCAATGG CAGTCAAAAG TTGCCAGTCC CTAAAGGAAT      180
TCAGGCCCCA TCAGGCCAAA GTATTACATT TGACCGAGCT GGGGGCAATT CGTCCCTGGC      240
TAAGGTTGAA TTTCAGACCA GTAAAGGAGC GATTGCTAT CAATTATATC TAGGAAATGG      300
AAAAATTAAA CGCATTAAGG AAACAAAAAA T      331

```

## (2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 110 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```

Ser Gly Ser Val Gln Ser Thr Phe Ser Ala Val Glu Glu Gln Ile Phe
1      5      10      15
Phe Met Glu Phe Glu Glu Leu Tyr Arg Glu Thr Gln Lys Arg Ser Val
20     25     30
Ala Ser Gln Gln Lys Thr Ser Leu Asn Leu Asp Gly Gln Thr Leu Ser
35     40     45
Asn Gly Ser Gln Lys Leu Pro Val Pro Lys Gly Ile Gln Ala Pro Ser
50     55     60
Gly Gln Ser Ile Thr Phe Asp Arg Ala Gly Gly Asn Ser Ser Leu Ala
65     70     75     80
Lys Val Glu Phe Gln Thr Ser Lys Gly Ala Ile Arg Tyr Gln Leu Tyr
85     90     95
Leu Gly Asn Gly Lys Ile Lys Arg Ile Lys Glu Thr Lys Asn
100    105    110

```

## (2) INFORMATION FOR SEQ ID NO: 145:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 196 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```

GGGACAAATT CAAAAAATA GGCAAGAGGA AGCAAAATC TTGCAAAAGG AAGAAGTCTT      60
GAGGGTAGCT AAGATGGCCC TGCAGACGGG GCAAAATCAG GTAAGCATCA ACGGAGTTGA      120

```

GATTCAGGTA TTTTCTAGTG AAAAAGGATT GGAGGTCTAC CATGGTTCAG AACAGTTGTT 180  
 GGCAATCAAA GAGCCA 196

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Gly Gln Ile Gln Lys Asn Arg Gln Glu Glu Ala Lys Ile Leu Gln Lys  
 1 5 10 15  
 Glu Glu Val Leu Arg Val Ala Lys Met Ala Leu Gln Thr Gly Gln Asn  
 20 25 30  
 Gln Val Ser Ile Asn Gly Val Glu Ile Gln Val Phe Ser Ser Glu Lys  
 35 40 45  
 Gly Leu Glu Val Tyr His Gly Ser Glu Gln Leu Leu Ala Ile Lys Glu  
 50 55 60  
 Pro  
 65

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

TCGCTACCAG CAACAAAGCG AGCAAAAGGA GTGGCTCTTG TTTGTGGACC AACTTGAGGT 60  
 AGAATTAGAC CGTTTCGAGT TCGAAAAAGT AGAAGGCAAT CGCCTATACA TGAAGCAAGA 120  
 TGGCAAGGAC ATCGCCATCG GTAAGTCAAA GTCAGATGAT TTCCGTAAAA CGAATGCTCG 180  
 TGGTCGAGGT TATCAGCCTA TGGTTTATGG ACTCAAATCT GTACGGATTA CAGAGGACAA 240  
 TCAACTGGTT CGCTTTCATT TCCAGTTCCA AAAAGGCTTA GAAAGGGAGT TCATCTATCG 300  
 TGTGGAAAAA GAAAAAAGT 319

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```

Arg Tyr Gln Gln Gln Ser Glu Gln Lys Glu Trp Leu Leu Phe Val Asp
1          5          10
Gln Leu Glu Val Glu Leu Asp Arg Ser Gln Phe Glu Lys Val Glu Gly
20          25          30
Asn Arg Leu Tyr Met Lys Gln Asp Gly Lys Asp Ile Ala Ile Gly Lys
35          40          45
Ser Lys Ser Asp Asp Phe Arg Lys Thr Asn Ala Arg Gly Arg Gly Tyr
50          55          60
Gln Pro Met Val Tyr Gly Leu Lys Ser Val Arg Ile Thr Glu Asp Asn
65          70          75          80
Gln Leu Val Arg Phe His Phe Gln Phe Gln Lys Gly Leu Glu Arg Glu
85          90          95
Phe Ile Tyr Arg Val Glu Lys Glu Lys Ser
100          105

```

(2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```

GAACCGACAA GTCGCCCACT ATCAAGACTA TGCTTTGAAT AAAGAAAAAT TGGTTGCTTT      60
TGCTATGGCT AAACGAACCA AAGATAAGGT TGAGCAAGAA AGTGGGGAAC AGTTTTTTTAA      120
TCTAGGTCAG GTAAGCTATC AAAACAAGAA AACTGGCTTA GTGACGAGGG TTCGTACGGA      180
TAAGAGCCAA TATGAGTTTC TGTTCCTTC AGTCAAAATC AAAGAAGAGA AAAGAGATAA      240
AAAGGAAGAG GTAGCGACCG ATTCAAGCGA AAAAGTGGAG AAGAAAAAAT CAGAAGAGAA      300
GCCTGAAAAG AAAGAGAATT CA  322

```

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```

Asn Arg Gln Val Ala His Tyr Gln Asp Tyr Ala Leu Asn Lys Glu Lys

```

|                                                                 |     |     |    |
|-----------------------------------------------------------------|-----|-----|----|
| 1                                                               | 5   | 10  | 15 |
| Leu Val Ala Phe Ala Met Ala Lys Arg Thr Lys Asp Lys Val Glu Gln | 20  | 25  | 30 |
| Glu Ser Gly Glu Gln Phe Phe Asn Leu Gly Gln Val Ser Tyr Gln Asn | 35  | 40  | 45 |
| Lys Lys Thr Gly Leu Val Thr Arg Val Arg Thr Asp Lys Ser Gln Tyr | 50  | 55  | 60 |
| Glu Phe Leu Phe Pro Ser Val Lys Ile Lys Glu Glu Lys Arg Asp Lys | 65  | 70  | 75 |
| Lys Glu Glu Val Ala Thr Asp Ser Ser Glu Lys Val Glu Lys Lys Lys | 85  | 90  | 95 |
| Ser Glu Glu Lys Pro Glu Lys Lys Glu Asn Ser                     | 100 | 105 |    |

## (2) INFORMATION FOR SEQ ID NO: 151:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 784 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GGTTGTCGGC TGGCAATATA TCCCGTTTCC ATCTAAAGGT AGTACAATTG GTCCTTACCC  | 60  |
| AAATGGTATC AGATTAGAAG GTTTTCCAAA GTCAGAGTGG TACTACTTCG ATAAAAATGG  | 120 |
| AGTGCTACAA GAGTTTGTGT GTTGGAAC ATTAGAGATT AAAACTAAAG ACAGTGTTGG    | 180 |
| AAGAAAGTAC GGGGAAAAAC GTGAAGATTC AGAAGATAAA GAAGAGAAGC GTTATTATAC  | 240 |
| GAAGTATTAC TTTAATCAAA ATCATTCTTT AGAGACAGGT TGGCTTTATG ATCAGTCTAA  | 300 |
| CTGGTATTAT CTAGCTAAGA CGGAAATTAA TGGAGAAAAC TACCTTGGTG GTGAAAGACG  | 360 |
| TGCGGGGTGG ATAAACGATG ATTCGACTTG GTACTACCTA GATCCAACAA CTGGTATTAT  | 420 |
| GCAAACAGGT TGGCAATATC TAGGTAATAA GTGGTACTAC CTCCGTTTCCT CAGGAGCAAT | 480 |
| GGCCACTGGC TGGTATCAGG AAGGTACCAC TTGGTATTAT TTAGACCACC CAAATGGCGA  | 540 |
| TATGAAAACA GGTTGGCAAA ACCTTGGGAA CAAATGGTAC TATCTCCGTT CATCAGGAGC  | 600 |
| TATGGCAACT GGTTGGTATC AAGATGGTTC AACTTGGTAC TACCTAAATG CAGGTAATGG  | 660 |
| AGACATGAAG ACAGGTTGGT TCCAGGTCAA TGGCAACTGG TACTATGCTT ATAGCTCAGG  | 720 |
| TGCTTTGGCA GTGAATACGA CCGTAGATGG CTATTCTGTC AACTATAATG GCGAATGGGT  | 780 |
| TCGG                                                               | 784 |

## (2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 261 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Gly | Trp | Gln | Tyr | Ile | Pro | Phe | Pro | Ser | Lys | Gly | Ser | Thr | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Pro | Tyr | Pro | Asn | Gly | Ile | Arg | Leu | Glu | Gly | Phe | Pro | Lys | Ser | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Tyr | Tyr | Phe | Asp | Lys | Asn | Gly | Val | Leu | Gln | Glu | Phe | Val | Gly | Trp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Thr | Leu | Glu | Ile | Lys | Thr | Lys | Asp | Ser | Val | Gly | Arg | Lys | Tyr | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Lys | Arg | Glu | Asp | Ser | Glu | Asp | Lys | Glu | Glu | Lys | Arg | Tyr | Tyr | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Tyr | Tyr | Phe | Asn | Gln | Asn | His | Ser | Leu | Glu | Thr | Gly | Trp | Leu | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Gln | Ser | Asn | Trp | Tyr | Tyr | Leu | Ala | Lys | Thr | Glu | Ile | Asn | Gly | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Tyr | Leu | Gly | Gly | Glu | Arg | Arg | Ala | Gly | Trp | Ile | Asn | Asp | Asp | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Trp | Tyr | Tyr | Leu | Asp | Pro | Thr | Thr | Gly | Ile | Met | Gln | Thr | Gly | Trp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Tyr | Leu | Gly | Asn | Lys | Trp | Tyr | Tyr | Leu | Arg | Ser | Ser | Gly | Ala | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Thr | Gly | Trp | Tyr | Gln | Glu | Gly | Thr | Thr | Trp | Tyr | Tyr | Leu | Asp | His |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Asn | Gly | Asp | Met | Lys | Thr | Gly | Trp | Gln | Asn | Leu | Gly | Asn | Lys | Trp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Tyr | Leu | Arg | Ser | Ser | Gly | Ala | Met | Ala | Thr | Gly | Trp | Tyr | Gln | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Ser | Thr | Trp | Tyr | Tyr | Leu | Asn | Ala | Gly | Asn | Gly | Asp | Met | Lys | Thr |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Trp | Phe | Gln | Val | Asn | Gly | Asn | Trp | Tyr | Tyr | Ala | Tyr | Ser | Ser | Gly |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |
| Ala | Leu | Ala | Val | Asn | Thr | Thr | Val | Asp | Gly | Tyr | Ser | Val | Asn | Tyr | Asn |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Glu | Trp | Val | Arg |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 260 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1708 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| GGCCAAATCA GAATGGGTAG AAGACAAGGG AGCCTTTTAT TATCTTGACC AAGATGGAAA | 60   |
| GATGAAAAGA AATGCTTGGG TAGGAACTTC CTATGTTGGT GCAACAGGTG CCAAAGTAAT | 120  |
| AGAAGACTGG GTCTATGATT CTCAATACGA TGCTTGTTT TATATCAAAG CAGATGGACA  | 180  |
| GCACGCAGAG AAAGAATGGC TCCAAATTAA AGGGAAGGAC TATTATTTCA AATCCGGTGG | 240  |
| TTATCTACTG ACAAGTCACT GGATTAATCA AGCTTATGTG AATGCTAGTG GTGCCAAAGT | 300  |
| ACAGCAAGGT TGGCTTTTTG ACAAACAATA CCAATCTTGG TTTTACATCA AAGAAAATGG | 360  |
| AAACTATGCT GATAAAGAAT GGATTTTCGA GAATGGTCAC TATTATTATC TAAAATCCGG | 420  |
| TGGCTACATG GCAGCCAATG AATGGATTTG GGATAAGGAA TCTTGTTTTT ATCTCAAATT | 480  |
| TGATGGGAAA ATGGCTGAAA AAGAATGGGT CTACGATTCT CATAGTCAAG CTTGGTACTA | 540  |
| CTTCAAATCC GGTGGTTACA TGACAGCCAA TGAATGGATT TGGGATAAGG AATCTTGGTT | 600  |
| TTATCTCAAA TCTGATGGGA AAATAGCTGA AAAAGAATGG GTCTACGATT CTCATAGTCA | 660  |
| AGCTTGGTAC TACTTCAAAT CCGGTGGTTA CATGACAGCC AATGAATGGA TTTGGGATAA | 720  |
| GGAATCTTGG TTTTACCTCA AATCTGATGG GAAAATAGCT GAAAAAGAAT GGGTCTACGA | 780  |
| TTCTCATAGT CAAGCTTGGT ACTACTTCAA ATCTGGTGGC TACATGGCGA AAAATGAGAC | 840  |
| AGTAGATGGT TATCAGCTTG GAAGCGATGG TAAATGGCTT GGAGGAAAAA CTACAAATGA | 900  |
| AAATGCTGCT TACTATCAAG TAGTGCCTGT TACAGCCAAT GTTTATGATT CAGATGGTGA | 960  |
| AAAGCTTTCC TATATATCGC AAGGTAGTGT CGTATGGCTA GATAAGGATA GAAAAAGTGA | 1020 |
| TGACAAGCGC TTGGCTATTA CTATTTCTGG TTTGTCAGGC TATATGAAAA CAGAAGATTT | 1080 |
| ACAAGCGCTA GATGCTAGTA AGGACTTTAT CCCTTATTAT GAGAGTGATG GCCACCGTTT | 1140 |
| TTATCACTAT GTGGCTCAGA ATGCTAGTAT CCCAGTAGCT TCTCATCTTT CTGATATGGA | 1200 |
| AGTAGGCAAG AAATATTATT CGGCAGATGG CCTGCATTTT GATGGTTTTA AGCTTGAGAA | 1260 |
| TCCCTTCCTT TTCAAAGATT TAACAGAGGC TACAACTAC AGTGCTGAAG AATTGGATAA  | 1320 |
| GGTATTTAGT TTGCTAAACA TTAACAATAG CCTTTTGGAG AACAAGGGCG CTACTTTTAA | 1380 |
| GGAAGCCGAA GAACATTACC ATATCAATGC TCTTTATCTC CTTGCCATA GTGCCCTAGA  | 1440 |
| AAGTAACTGG GGAAGAAGTA AAATTGCCAA AGATAAGAAT AATTTCTTTG GCATTACAGC | 1500 |
| CTATGATACG ACCCCTTACC TTTCTGCTAA GACATTTGAT GATGTGGATA AGGGAATTTT | 1560 |
| AGGTGCAACC AAGTGGATTA AGGAAAATTA TATCGATAGG GGAAGAACTT TCCTTGAAAA | 1620 |
| CAAGGCTTCT GGTATGAATG TGAATATGC TTCAGACCCT TATTGGGGCG AAAAAATTGC  | 1680 |

TAGTGTGATG ATGAAAATCA ATGAGAAAG

1708

## (2) INFORMATION FOR SEQ ID NO:154:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Ala Lys Ser Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp  
 1 5 10 15

Gln Asp Gly Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val  
 20 25 30

Gly Ala Thr Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln  
 35 40 45

Tyr Asp Ala Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys  
 50 55 60

Glu Trp Leu Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly  
 65 70 75 80

Tyr Leu Leu Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser  
 85 90 95

Gly Ala Lys Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser  
 100 105 110

Trp Phe Tyr Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile  
 115 120 125

Phe Glu Asn Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala  
 130 135 140

Ala Asn Glu Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Phe  
 145 150 155 160

Asp Gly Lys Met Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln  
 165 170 175

Ala Trp Tyr Tyr Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp  
 180 185 190

Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile  
 195 200 205

Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr  
 210 215 220

Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp Ile Trp Asp Lys  
 225 230 235 240

Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile Ala Glu Lys Glu  
 245 250 255

Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr Phe Lys Ser Gly

| 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Tyr | Met | Ala | Lys | Asn | Glu | Thr | Val | Asp | Gly | Tyr | Gln | Leu | Gly | Ser |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Gly | Lys | Trp | Leu | Gly | Gly | Lys | Thr | Thr | Asn | Glu | Asn | Ala | Ala | Tyr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Tyr | Gln | Val | Val | Pro | Val | Thr | Ala | Asn | Val | Tyr | Asp | Ser | Asp | Gly | Glu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Lys | Leu | Ser | Tyr | Ile | Ser | Gln | Gly | Ser | Val | Val | Trp | Leu | Asp | Lys | Asp |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Arg | Lys | Ser | Asp | Asp | Lys | Arg | Leu | Ala | Ile | Thr | Ile | Ser | Gly | Leu | Ser |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Tyr | Met | Lys | Thr | Glu | Asp | Leu | Gln | Ala | Leu | Asp | Ala | Ser | Lys | Asp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Phe | Ile | Pro | Tyr | Tyr | Glu | Ser | Asp | Gly | His | Arg | Phe | Tyr | His | Tyr | Val |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Gln | Asn | Ala | Ser | Ile | Pro | Val | Ala | Ser | His | Leu | Ser | Asp | Met | Glu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Val | Gly | Lys | Lys | Tyr | Tyr | Ser | Ala | Asp | Gly | Leu | His | Phe | Asp | Gly | Phe |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Lys | Leu | Glu | Asn | Pro | Phe | Leu | Phe | Lys | Asp | Leu | Thr | Glu | Ala | Thr | Asn |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Tyr | Ser | Ala | Glu | Glu | Leu | Asp | Lys | Val | Phe | Ser | Leu | Leu | Asn | Ile | Asn |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |
| Asn | Ser | Leu | Leu | Glu | Asn | Lys | Gly | Ala | Thr | Phe | Lys | Glu | Ala | Glu | Glu |
|     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| His | Tyr | His | Ile | Asn | Ala | Leu | Tyr | Leu | Leu | Ala | His | Ser | Ala | Leu | Glu |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Ser | Asn | Trp | Gly | Arg | Ser | Lys | Ile | Ala | Lys | Asp | Lys | Asn | Asn | Phe | Phe |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Gly | Ile | Thr | Ala | Tyr | Asp | Thr | Thr | Pro | Tyr | Leu | Ser | Ala | Lys | Thr | Phe |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Asp | Asp | Val | Asp | Lys | Gly | Ile | Leu | Gly | Ala | Thr | Lys | Trp | Ile | Lys | Glu |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Asn | Tyr | Ile | Asp | Arg | Gly | Arg | Thr | Phe | Leu | Gly | Asn | Lys | Ala | Ser | Gly |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Met | Asn | Val | Glu | Tyr | Ala | Ser | Asp | Pro | Tyr | Trp | Gly | Glu | Lys | Ile | Ala |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Ser | Val | Met | Met | Lys | Ile | Asn | Glu | Lys |     |     |     |     |     |     |     |
|     |     |     |     | 565 |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 946 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ATTTCGAGAT GATTCTGAAG GATGGCAGTT TGTCCAAGAA AATGGTAGAA CCTACTACAA   | 60  |
| AAAGGGGGAT CTAAAAGAAA CCTACTGGAG AGTGATAGAT GGGAAGTACT ATTATTTTGA   | 120 |
| TCCTTTATCC GGAGAGATGG TTGTCGGCTG GCAATATATA CCTGCTCCAC ACAAGGGGGT   | 180 |
| TACGATTGGT CCTTCTCCAA GAATAGAGAT TGCTCTTAGA CCAGATTGGT TTTATTTTGG   | 240 |
| TCAAGATGGT GTATTACAAG AATTTGTTGG CAAGCAAGTT TTAGAAGCAA AAAGTCTGCTAC | 300 |
| GAATACCAAC AAACATCATG GGAAGAATA TGATAGCCAA GCAGAGAAAC GAGTCTATTA    | 360 |
| TTTTGAAGAT CAGCGTAGTT ATCATACTTT AAAAAGTGGT TGGATTTATG AAGAGGGTCA   | 420 |
| TTGGTATTAT TTACAGAAGG ATGGTGGCTT TGATTCGCGC ATCAACAGAT TGACGGTTGG   | 480 |
| AGAGCTAGCA CGTGGTTGGG TTAAGGATTA CCCTCTTACG TATGATGAAG AGAAGCTAAA   | 540 |
| AGCAGCTCCA TGGTACTATC TAAATCCAGC AACTGGCATT ATGCAAACAG GTTGGCAATA   | 600 |
| TCTAGGTAAT AGATGGTACT ACCTCCATTC GTCAGGAGCT ATGGCAACTG GCTGGTATAA   | 660 |
| GGAAGGCTCA ACTTGGTACT ATCTAGATGC TGAAAATGGT GATATGAGAA CTGGCTGGCA   | 720 |
| AAACCTTGGG AACAAATGGT ACTATCTCCG TTCATCAGGA GCTATGGCAA CTGGTTGGTA   | 780 |
| TCAGGAAAGT TCGACTTGGT ACTATCTAAA TGCAAGTAAT GGAGATATGA AAACAGGCTG   | 840 |
| GTTCCAAGTC AATGGTAACT GGTACTATGC CTATGATTCA GGTGCTTTAG CTGTTAATAC   | 900 |
| CACAGTAGGT GGTACTACT TAACTATAA TGGTGAATGG GTTAAG                    | 946 |

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 316 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Phe | Ala | Asp | Asp | Ser | Glu | Gly | Trp | Gln | Phe | Val | Gln | Glu | Asn | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Arg | Thr | Tyr | Tyr | Lys | Lys | Gly | Asp | Leu | Lys | Glu | Thr | Tyr | Trp | Arg | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ile | Asp | Gly | Lys | Tyr | Tyr | Tyr | Phe | Asp | Pro | Leu | Ser | Gly | Glu | Met | Val |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Gly | Trp | Gln | Tyr | Ile | Pro | Ala | Pro | His | Lys | Gly | Val | Thr | Ile | Gly |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |

Pro Ser Pro Arg Ile Glu Ile Ala Leu Arg Pro Asp Trp Phe Tyr Phe  
 65 70 75 80  
 Gly Gln Asp Gly Val Leu Gln Glu Phe Val Gly Lys Gln Val Leu Glu  
 85 90 95  
 Ala Lys Thr Ala Thr Asn Thr Asn Lys His His Gly Glu Glu Tyr Asp  
 100 105 110  
 Ser Gln Ala Glu Lys Arg Val Tyr Tyr Phe Glu Asp Gln Arg Ser Tyr  
 115 120 125  
 His Thr Leu Lys Thr Gly Trp Ile Tyr Glu Glu Gly His Trp Tyr Tyr  
 130 135 140  
 Leu Gln Lys Asp Gly Gly Phe Asp Ser Arg Ile Asn Arg Leu Thr Val  
 145 150 155 160  
 Gly Glu Leu Ala Arg Gly Trp Val Lys Asp Tyr Pro Leu Thr Tyr Asp  
 165 170 175  
 Glu Glu Lys Leu Lys Ala Ala Pro Trp Tyr Tyr Leu Asn Pro Ala Thr  
 180 185 190  
 Gly Ile Met Gln Thr Gly Trp Gln Tyr Leu Gly Asn Arg Trp Tyr Tyr  
 195 200 205  
 Leu His Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Lys Glu Gly Ser  
 210 215 220  
 Thr Trp Tyr Tyr Leu Asp Ala Glu Asn Gly Asp Met Arg Thr Gly Trp  
 225 230 235 240  
 Gln Asn Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met  
 245 250 255  
 Ala Thr Gly Trp Tyr Gln Glu Ser Ser Thr Trp Tyr Tyr Leu Asn Ala  
 260 265 270  
 Ser Asn Gly Asp Met Lys Thr Gly Trp Phe Gln Val Asn Gly Asn Trp  
 275 280 285  
 Tyr Tyr Ala Tyr Asp Ser Gly Ala Leu Ala Val Asn Thr Thr Val Gly  
 290 295 300  
 Gly Tyr Tyr Leu Asn Tyr Asn Gly Glu Trp Val Lys  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1415 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

TGTCGCTGCA AATGAACTG AAGTAGCAA AACTTCGCAG GATACAACGA CAGCTTCAAG 60  
 TAGTTCAGAG CAAAATCAGT CTTCTAATAA AACGCAAACG AGCGCAGAAG TACAGACTAA 120

```

TGCTGCTGCC CACTGGGATG GGGATTATTA TGTAAGGAT GATGGTTCTA AAGCTCAAAG      180
TGAATGGATT TTTGACAAC ACTATAAGGC TTGGTTTTAT ATTAATTCAG ATGGTCGTTA      240
CTCGCAGAAT GAATGGCATG GAAATTACTA CCTGAAATCA GGTGGATATA TGGCCCCAAA      300
CGAGTGGATC TATGACAGTA ATTACAAGAG TTGGTTTTAT CTCAAGTCAG ATGGGGCTTA      360
TGCTCATCAA GAATGGCAAT TGATTGGAAA TAAGTGGTAC TACTTCAAGA AGTGGGGTTA      420
CATGGCTAAA AGCCAATGGC AAGGAAGTTA TTTCTTGAAT GGTCAAGGAG CTATGATGCA      480
AAATGAATGG CTSCTATGAT CCAGCCTATT CTGCTTATTT TTATCTAAAA TCCGATGGAA      540
CTTATGCTAA CCAAGAGTGG CAAAAGTGG GCGGCAAATG GTACTATTTT AAGAAGTGGG      600
GCTATATGGC TCGGAATGAG TGGCAAGGCA ACTACTATTT GACTGGAAGT GGTGCCATGG      660
CGACTGACGA AGTGATTATG GATGGTACTC GCTATATCTT TCGGCCTCT GGTGAGCTCA      720
AAGAAAAAAA AGATTTGAAT GTCGGCTGGG TTCACAGAGA TGGTAAGCGC TATTTCTTTA      780
ATAATAGAGA AGAACAAGTG GGAACCGAAC ATGCTAAGAA AGTCATTGAT ATTAGTGAGC      840
ACAATGGTCG TATCAATGAT TGGAAAAAGG TTATTGATGA GAACGAAGTG GATGGTGTCA      900
TTGTTCTGCT AGGTTATAGC GGTAAAGAAG ACAAGGAATT GCGGCATAAC ATTAAGGAGT      960
TAAACCGTCT GGAATTCCT TATGGTGTCT ATCTCTATAC CTATGCTGAA AATGAGACCG     1020
ATGCTGAGAG TGACGCTAAA CAGACCATTG AACTTATAAA GAAATACAAT ATGAACCTGT     1080
CTTACCCTAT CTATTATGAT GTTGAGAATT GGAATATGT AAATAAGAGC AAGAGAGCTC     1140
CAAGTGATAC AGGCACTTGG GTTAAAATCA TCAACAAGTA CATGGACACG ATGAAGCAGG     1200
CGGGTTATCA AAATGTGTAT GTCTATAGCT ATCGTAGTTT ATTACAGACG CGTTTAAAC      1260
ACCCAGATAT TTTAAACAT GTAAACTGGG TAGCGGCCTA TACGAATGCT TTAGAATGGG      1320
AAAACCCTCA TTATTCAGGA AAAAAAGGTT GGCAATATAC CTCTTCTGAA TACATGAAAG      1380
GAATCCAAGG GCGCGTAGAT GTCAGCGTTT GGTAT                                1415

```

## (2) INFORMATION FOR SEQ ID NO:158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

```

Val Ala Ala Asn Glu Thr Glu Val Ala Lys Thr Ser Gln Asp Thr Thr
1          5          10          15

Thr Ala Ser Ser Ser Glu Gln Asn Gln Ser Ser Asn Lys Thr Gln
20        25        30

Thr Ser Ala Glu Val Gln Thr Asn Ala Ala Ala His Trp Asp Gly Asp

```

| 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Val | Lys | Asp | Asp | Gly | Ser | Lys | Ala | Gln | Ser | Glu | Trp | Ile | Phe |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Asn | Tyr | Tyr | Lys | Ala | Trp | Phe | Tyr | Ile | Asn | Ser | Asp | Gly | Arg | Tyr |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Gln | Asn | Glu | Trp | His | Gly | Asn | Tyr | Tyr | Leu | Lys | Ser | Gly | Gly | Tyr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Ala | Gln | Asn | Glu | Trp | Ile | Tyr | Asp | Ser | Asn | Tyr | Lys | Ser | Trp | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Leu | Lys | Ser | Asp | Gly | Ala | Tyr | Ala | His | Gln | Glu | Trp | Gln | Leu | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Asn | Lys | Trp | Tyr | Tyr | Phe | Lys | Lys | Trp | Gly | Tyr | Met | Ala | Lys | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Trp | Gln | Gly | Ser | Tyr | Phe | Leu | Asn | Gly | Gln | Gly | Ala | Met | Met | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Glu | Trp | Leu | Tyr | Asp | Pro | Ala | Tyr | Ser | Ala | Tyr | Phe | Tyr | Leu | Lys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Asp | Gly | Thr | Tyr | Ala | Asn | Gln | Glu | Trp | Gln | Lys | Val | Gly | Gly | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Trp | Tyr | Tyr | Phe | Lys | Lys | Trp | Gly | Tyr | Met | Ala | Arg | Asn | Glu | Trp | Gln |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Asn | Tyr | Tyr | Leu | Thr | Gly | Ser | Gly | Ala | Met | Ala | Thr | Asp | Glu | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Met | Asp | Gly | Thr | Arg | Tyr | Ile | Phe | Ala | Ala | Ser | Gly | Glu | Leu | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Lys | Lys | Asp | Leu | Asn | Val | Gly | Trp | Val | His | Arg | Asp | Gly | Lys | Arg |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Tyr | Phe | Phe | Asn | Asn | Arg | Glu | Glu | Gln | Val | Gly | Thr | Glu | His | Ala | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Lys | Val | Ile | Asp | Ile | Ser | Glu | His | Asn | Gly | Arg | Ile | Asn | Asp | Trp | Lys |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Val | Ile | Asp | Glu | Asn | Glu | Val | Asp | Gly | Val | Ile | Val | Arg | Leu | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Tyr | Ser | Gly | Lys | Glu | Asp | Lys | Glu | Leu | Ala | His | Asn | Ile | Lys | Glu | Leu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Asn | Arg | Leu | Gly | Ile | Pro | Tyr | Gly | Val | Tyr | Leu | Tyr | Thr | Tyr | Ala | Glu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asn | Glu | Thr | Asp | Ala | Glu | Ser | Asp | Ala | Lys | Gln | Thr | Ile | Glu | Leu | Ile |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Lys | Lys | Tyr | Asn | Met | Asn | Leu | Ser | Tyr | Pro | Ile | Tyr | Tyr | Asp | Val | Glu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Asn | Trp | Glu | Tyr | Val | Asn | Lys | Ser | Lys | Arg | Ala | Pro | Ser | Asp | Thr | Gly |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |

Thr Trp Val Lys Ile Ile Asn Lys Tyr Met Asp Thr Met Lys Gln Ala  
 385 390 395 400  
 Gly Tyr Gln Asn Val Tyr Val Tyr Ser Tyr Arg Ser Leu Leu Gln Thr  
 405 410 415  
 Arg Leu Lys His Pro Asp Ile Leu Lys His Val Asn Trp Val Ala Ala  
 420 425 430  
 Tyr Thr Asn Ala Leu Glu Trp Glu Asn Pro His Tyr Ser Gly Lys Lys  
 435 440 445  
 Gly Trp Gln Tyr Thr Ser Ser Glu Tyr Met Lys Gly Ile Gln Gly Arg  
 450 455 460  
 Val Asp Val Ser Val Trp Tyr  
 465 470

## (2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1924 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TACGTCTCAG CCTACTTTTG TAAGAGCAGA AGAATCTCCA CAAGTTGTCG AAAAATCTTC  | 60   |
| ATTAGAGAAG AAATATGAGG AAGCAAAAGC AAAAGCTGAT ACTGCCAAGA AAGATTACGA  | 120  |
| AACGGCTAAA AAGAAAGCAG AAGACGCTCA GAAAAAGTAT GAAGATGATC AGAAGAGAAC  | 180  |
| TGAGGAGAAA GCTCGAAAAG AAGCAGAAGC ATCTCAAAAA TTGAATGATG TGGCGCTTGT  | 240  |
| TGTTCAAAAT GCATATAAAG AGTACCGAGA AGTTCAAAAT CAACGTAGTA AATATAAATC  | 300  |
| TGACGCTGAA TATCAGAAAA AATTAACAGA GGTGCGACTCT AAAATAGAGA AGGCTAGGAA | 360  |
| AGAGCAACAG GACTTGCAAA ATAAATTTAA TGAAGTAAGA GCAGTTGTAG TTCCTGAACC  | 420  |
| AAATGCGTTG GCTGAGACTA AGAAAAAGC AGAAGAAGCT AAAGCAGAAG AAAAAGTAGC   | 480  |
| TAAGAGAAAA TATGATTATG CAACTCTAAA GGTAGCACTA GCGAAGAAAG AAGTAGAGGC  | 540  |
| TAAGGAAGTT GAAATTGAAA AACTTCAATA TGAAATTTCT ACTTTGGAAC AAGAAGTTGC  | 600  |
| TACTGCTCAA CATCAAGTAG ATAATTTGAA AAACTTCTT GCTGGTGCGG ATCCTGATGA   | 660  |
| TGGCACAGAA GTTATAGAAG CTAAATTTAA AAAAGGAGAA GCTGAGCTAA ACGCTAAACA  | 720  |
| AGCTGAGTTA GCAAAAAAAC AAACAGAACT TGAAAACTT CTTGACAGCC TTGATCCTGA   | 780  |
| AGGTAAGACT CAGGATGAAT TAGATAAAGA AGCAGAAGAA GCTGAGTTGG ATAAAAAGC   | 840  |
| TGATGAAGTT CAAAATAAAG TTGCTGATTT AGAAAAAGAA ATTAGTAACC TTGAAATATT  | 900  |
| ACTTGGAGGG GCTGATNCTG AAGATGATAC TGCTGCTCTT CAAAATAAAT TAGCTACTAA  | 960  |
| AAAAGCTGAA TTGGAAAAAA CTCAAAAAGA ATTAGATGCA GCTCTTAATG AGTTAGGCCC  | 1020 |

```

TGATGGAGAT GAAGAAGAAA CTCCAGCGCC GGCTCCTCAA CCAGAGCAAC CAGCTCCTGC      1080
ACCAAAACCA GAGCAACCAG CTCCAGCTCC AAAACCAGAG CAACCAGCTC CTGCACCAAA      1140
ACCAGAGCAA CCAGCTCCAG CTCCAAAACC AGAGCAACCA GCTCCAGCTC CAAAACCAGA      1200
GCAACCAGCT AAGCCGGAGA AACCAGCTGA AGAGCCTACT CAACCAGAAA AACCAGCCAC      1260
TCCAAAAACA GGCTGGAAAC AAGAAAACGG TATGTGGTAT TTCTACAATA CTGATGGTTC      1320
AATGGCAATA GGTGGGCTCC AAAACAACGG TTCATGGTAC TACCTAAACG CTAACGGCGC      1380
TATGGCAACA GGTGGGTGA AAGATGGAGA TACCTGGTAC TATCTTGAAG CATCAGGTGC      1440
TATGAAAGCA AGCCAATGGT TCAAAGTATC AGATAAATGG TACTATGTCA ACAGCAATGG      1500
CGCTATGGCG ACAGGCTGGC TCCAATACAA TGGCTCATGG TACTACCTCA ACGCTAATGG      1560
TGATATGGCG ACAGGATGGC TCCAATACAA CGGTTTCATGG TATTACCTCA ACGCTAATGG      1620
TGATATGGCG ACAGGATGGG CTAAAGTCAA CGGTTTCATGG TACTACCTAA ACGCTAACGG      1680
TGCTATGGCT ACAGGTTGGG CTAAAGTCAA CGGTTTCATGG TACTACCTAA ACGCTAACGG      1740
TTCAATGGCA ACAGGTTGGG TGAAAGATGG AGATACCTGG TACTATCTTG AAGCATCAGG      1800
TGCTATGAAA GCAAGCCAAT GGTTCAAAGT ATCAGATAAA TGGTACTATG TCAATGGCTT      1860
AGGTGCCCTT GCAGTCAACA CAACTGTAGA TGGCTATAAA GTCAATGCCA ATGGTGAATG      1920
GGTT  1924

```

## (2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 641 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

Thr Ser Gln Pro Thr Phe Val Arg Ala Glu Glu Ser Pro Gln Val Val
1          5          10          15
Glu Lys Ser Ser Leu Glu Lys Lys Tyr Glu Glu Ala Lys Ala Lys Ala
20          25          30
Asp Thr Ala Lys Lys Asp Tyr Glu Thr Ala Lys Lys Lys Ala Glu Asp
35          40          45
Ala Gln Lys Lys Tyr Glu Asp Asp Gln Lys Arg Thr Glu Glu Lys Ala
50          55          60
Arg Lys Glu Ala Glu Ala Ser Gln Lys Leu Asn Asp Val Ala Leu Val
65          70          75          80
Val Gln Asn Ala Tyr Lys Glu Tyr Arg Glu Val Gln Asn Gln Arg Ser
85          90          95

```

Lys Tyr Lys Ser Asp Ala Glu Tyr Gln Lys Lys Leu Thr Glu Val Asp  
 100 105 110  
 Ser Lys Ile Glu Lys Ala Arg Lys Glu Gln Gln Asp Leu Gln Asn Lys  
 115 120 125  
 Phe Asn Glu Val Arg Ala Val Val Val Pro Glu Pro Asn Ala Leu Ala  
 130 135 140  
 Glu Thr Lys Lys Lys Ala Glu Glu Ala Lys Ala Glu Glu Lys Val Ala  
 145 150 155 160  
 Lys Arg Lys Tyr Asp Tyr Ala Thr Leu Lys Val Ala Leu Ala Lys Lys  
 165 170 175  
 Glu Val Glu Ala Lys Glu Leu Glu Ile Glu Lys Leu Gln Tyr Glu Ile  
 180 185 190  
 Ser Thr Leu Glu Gln Glu Val Ala Thr Ala Gln His Gln Val Asp Asn  
 195 200 205  
 Leu Lys Lys Leu Leu Ala Gly Ala Asp Pro Asp Asp Gly Thr Glu Val  
 210 215 220  
 Ile Glu Ala Lys Leu Lys Lys Gly Glu Ala Glu Leu Asn Ala Lys Gln  
 225 230 235 240  
 Ala Glu Leu Ala Lys Lys Gln Thr Glu Leu Glu Lys Leu Leu Asp Ser  
 245 250 255  
 Leu Asp Pro Glu Gly Lys Thr Gln Asp Glu Leu Asp Lys Glu Ala Glu  
 260 265 270  
 Glu Ala Glu Leu Asp Lys Lys Ala Asp Glu Leu Gln Asn Lys Val Ala  
 275 280 285  
 Asp Leu Glu Lys Glu Ile Ser Asn Leu Glu Ile Leu Leu Gly Gly Ala  
 290 295 300  
 Asp Xaa Glu Asp Asp Thr Ala Ala Leu Gln Asn Lys Leu Ala Thr Lys  
 305 310 315 320  
 Lys Ala Glu Leu Glu Lys Thr Gln Lys Glu Leu Asp Ala Ala Leu Asn  
 325 330 335  
 Glu Leu Gly Pro Asp Gly Asp Glu Glu Glu Thr Pro Ala Pro Ala Pro  
 340 345 350  
 Gln Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro  
 355 360 365  
 Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro  
 370 375 380  
 Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu  
 385 390 395 400  
 Gln Pro Ala Lys Pro Glu Lys Pro Ala Glu Glu Pro Thr Gln Pro Glu  
 405 410 415  
 Lys Pro Ala Thr Pro Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp  
 420 425 430  
 Tyr Phe Tyr Asn Thr Asp Gly Ser Met Ala Ile Gly Trp Leu Gln Asn

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 435                                                             | 440 | 445 |
| Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly |     |     |
| 450                                                             | 455 | 460 |
| Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala |     |     |
| 465                                                             | 470 | 475 |
| Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val |     |     |
|                                                                 | 485 | 490 |
| Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser |     |     |
|                                                                 | 500 | 505 |
| Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Leu Gln |     |     |
|                                                                 | 515 | 520 |
| Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr |     |     |
|                                                                 | 530 | 535 |
| Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly |     |     |
| 545                                                             | 550 | 555 |
| Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu |     |     |
|                                                                 | 565 | 570 |
| Asn Ala Asn Gly Ser Met Ala Thr Gly Trp Val Lys Asp Gly Asp Thr |     |     |
|                                                                 | 580 | 585 |
| Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser Gln Trp Phe |     |     |
|                                                                 | 595 | 600 |
| Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Leu Gly Ala Leu Ala |     |     |
|                                                                 | 610 | 615 |
| Val Asn Thr Thr Val Asp Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp |     |     |
| 625                                                             | 630 | 635 |
| Val                                                             |     |     |

## (2) INFORMATION FOR SEQ ID NO: 161:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 670 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TGGACAGGTG AAAGGTCATG CTACATTTGT GAAATCCATG ACAACTGAAA TGTACCAAGA | 60  |
| ACAACAGAAC CATTCTCTCG CCTACAATCA ACGCTTGGNT TCGCAAAATC GCATTGTAGA | 120 |
| TCCTTTTTTG GCGGAGGGAT ATGAGGTCAA TTACCAAGTG TCTGACGACC CTGATGCAGT | 180 |
| CTATGGTTAC TTGTCTATTC CAAGTTTGGA AATCATGGAG CCGGTTTATT TGGGAGCAGA | 240 |
| TTATCATCAT TTAGGGATGG GCTTGGCTCA TGTGGATGGT ACACCGCTGC CTCTGGATGG | 300 |
| TACAGGGATT CGCTCAGTGA TTGCTGGGCA CCGTGCAGAG CCAAGCCATG TCTTTTCCG  | 360 |

CCATTTGGAT CAGCTAAAAG TTGGAGATGC TCTTTATTAT GATAATGGCC AGGAAATTGT 420  
 AGAATATCAG ATGATGGACA CAGAGATTAT TTTACCGTCG GAATGGGAAA AATTAGAATC 480  
 GGTTAGCTCT AAAAATATCA TGACCTTGAT AACCTGCGAT CCGATTCTTA CCTTTAATAA 540  
 ACGCTTATTA GTGAATTTTG AACGAGTCGC TGTTTATCAA AAATCAGATC CACAAACAGC 600  
 TGCAGTTGCG AGGGTTGCTT TTACGAAAGA AGGACAATCT GTATCGCGTG TTGCAACCTC 660  
 TCAATGGTTG 670

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 223 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gln | Val | Lys | Gly | His | Ala | Thr | Phe | Val | Lys | Ser | Met | Thr | Thr | Glu | 1   | 5   | 10  | 15  |
| Met | Tyr | Gln | Glu | Gln | Gln | Asn | His | Ser | Leu | Ala | Tyr | Asn | Gln | Arg | Leu | 20  | 25  | 30  |     |
| Xaa | Ser | Gln | Asn | Arg | Ile | Val | Asp | Pro | Phe | Leu | Ala | Glu | Gly | Tyr | Glu | 35  | 40  | 45  |     |
| Val | Asn | Tyr | Gln | Val | Ser | Asp | Asp | Pro | Asp | Ala | Val | Tyr | Gly | Tyr | Leu | 50  | 55  | 60  |     |
| Ser | Ile | Pro | Ser | Leu | Glu | Ile | Met | Glu | Pro | Val | Tyr | Leu | Gly | Ala | Asp | 65  | 70  | 75  | 80  |
| Tyr | His | His | Leu | Gly | Met | Gly | Leu | Ala | His | Val | Asp | Gly | Thr | Pro | Leu | 85  | 90  | 95  |     |
| Pro | Leu | Asp | Gly | Thr | Gly | Ile | Arg | Ser | Val | Ile | Ala | Gly | His | Arg | Ala | 100 | 105 | 110 |     |
| Glu | Pro | Ser | His | Val | Phe | Phe | Arg | His | Leu | Asp | Gln | Leu | Lys | Val | Gly | 115 | 120 | 125 |     |
| Asp | Ala | Leu | Tyr | Tyr | Asp | Asn | Gly | Gln | Glu | Ile | Val | Glu | Tyr | Gln | Met | 130 | 135 | 140 |     |
| Met | Asp | Thr | Glu | Ile | Ile | Leu | Pro | Ser | Glu | Trp | Glu | Lys | Leu | Glu | Ser | 145 | 150 | 155 | 160 |
| Val | Ser | Ser | Lys | Asn | Ile | Met | Thr | Leu | Ile | Thr | Cys | Asp | Pro | Ile | Pro | 165 | 170 | 175 |     |
| Thr | Phe | Asn | Lys | Arg | Leu | Leu | Val | Asn | Phe | Glu | Arg | Val | Ala | Val | Tyr | 180 | 185 | 190 |     |
| Gln | Lys | Ser | Asp | Pro | Gln | Thr | Ala | Ala | Val | Ala | Arg | Val | Ala | Phe | Thr | 195 | 200 | 205 |     |

Lys Glu Gly Gln Ser Val Ser Arg Val Ala Thr Ser Gln Trp Leu  
 210 215 220

## (2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 784 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GATTGCTCCT TTGAAGGATT TGAGAGAAAC CATGTTGGAA ATTGCTTCTG GTGCTCAAAA  | 60  |
| TCTTCGTGCC AAGGAAGTTG GTGCCTATGA ACTGAGAGAA GTAACCTGCC AATTTAATGC  | 120 |
| TATGTTGGAT CAGATTGATC AGTTGATGGT AGCTATTCTG AGCCAGGAAG AAACGACCCG  | 180 |
| TCAGTACCAA CTTCAAGCCC TTTCGAGCCA GATTAATCCA CATTTCCCTCT ATAACACTTT | 240 |
| GGACACCATC ATCTGGATGG CTGAATTTCA TGATAGTCAG CGAGTGGTGC AGGTGACCAA  | 300 |
| GTCCTTGGCA ACCTATTTCC GCTTGGCGCT CAATCAAGGC AAGGACTTGA TTTGTCTCTC  | 360 |
| TGACGAAATC AATCATGTCC GCCAGTATCT CTTTATCCAG AAACAACGCT ATGGAGATAA  | 420 |
| GCTGGAATAC GAAATTAATG AAAATGTTGC CTTTGATAAT TTAGTCTTAC CCAAGCTGGT  | 480 |
| CCTACAACCC CTTGTAGAAA ATGCTCTTTA CCATGGCATT AAGGAAAAGG AAGGTCAGGG  | 540 |
| CCATATTAAA CTTTCTGTCC AGAAACAGGA TTCGGGATTG GTCATCCGTA TTGAGGATGA  | 600 |
| TGGCGTTGGC TTCCAAGATG CTGGTGATAG TAGTCAAAGT CAACTCAAAC GTGGGGGAGT  | 660 |
| TGGTCTTCAA AATGTCGATC AACGGCTCAA ACTTCATTTT GGAGCCAATT ACCATATGAA  | 720 |
| GATTGATTCT AGACCCCAAA AAGGGACGAA AGTTGAAATA TATATAAATA GAATAGAAAC  | 780 |
| TAGC                                                               | 784 |

## (2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 261 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ile Ala Pro Leu Lys Asp Leu Arg Glu Thr Met Leu Glu Ile Ala Ser |  |
| 1 5 10 15                                                       |  |
| Gly Ala Gln Asn Leu Arg Ala Lys Glu Val Gly Ala Tyr Glu Leu Arg |  |
| 20 25 30                                                        |  |
| Glu Val Thr Arg Gln Phe Asn Ala Met Leu Asp Gln Ile Asp Gln Leu |  |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| Met Val Ala Ile Arg Ser Gln Glu Glu Thr Thr Arg Gln Tyr Gln Leu |     |     |
| 50                                                              | 55  | 60  |
| Gln Ala Leu Ser Ser Gln Ile Asn Pro His Phe Leu Tyr Asn Thr Leu |     |     |
| 65                                                              | 70  | 75  |
| Asp Thr Ile Ile Trp Met Ala Glu Phe His Asp Ser Gln Arg Val Val |     |     |
|                                                                 | 85  | 90  |
| Gln Val Thr Lys Ser Leu Ala Thr Tyr Phe Arg Leu Ala Leu Asn Gln |     |     |
|                                                                 | 100 | 105 |
| Gly Lys Asp Leu Ile Cys Leu Ser Asp Glu Ile Asn His Val Arg Gln |     |     |
|                                                                 | 115 | 120 |
| Tyr Leu Phe Ile Gln Lys Gln Arg Tyr Gly Asp Lys Leu Glu Tyr Glu |     |     |
|                                                                 | 130 | 135 |
| Ile Asn Glu Asn Val Ala Phe Asp Asn Leu Val Leu Pro Lys Leu Val |     |     |
|                                                                 | 145 | 150 |
| Leu Gln Pro Leu Val Glu Asn Ala Leu Tyr His Gly Ile Lys Glu Lys |     |     |
|                                                                 | 165 | 170 |
| Glu Gly Gln Gly His Ile Lys Leu Ser Val Gln Lys Gln Asp Ser Gly |     |     |
|                                                                 | 180 | 185 |
| Leu Val Ile Arg Ile Glu Asp Asp Gly Val Gly Phe Gln Asp Ala Gly |     |     |
|                                                                 | 195 | 200 |
| Asp Ser Ser Gln Ser Gln Leu Lys Arg Gly Gly Val Gly Leu Gln Asn |     |     |
|                                                                 | 210 | 215 |
| Val Asp Gln Arg Leu Lys Leu His Phe Gly Ala Asn Tyr His Met Lys |     |     |
|                                                                 | 225 | 230 |
| Ile Asp Ser Arg Pro Gln Lys Gly Thr Lys Val Glu Ile Tyr Ile Asn |     |     |
|                                                                 | 245 | 250 |
| Arg Ile Glu Thr Ser                                             |     |     |
|                                                                 | 260 |     |

## (2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGGCTC CATAATATCT ATAAGGGATT | 60  |
| TACCCACTAC AAATATTATA GAGCCGAAAA TTCACATCTA ATATATGCAG ACTACTTTGA | 120 |
| AATGAAATTA AAAAAATTAT TAAAGGATGA CACAAAAGTT TTTGAAAAAT CTACATTCAA | 180 |
| ATTTGTAGAA GGATATAAAA TATACCTGAC AGAATCTAAA GAATCTGGAA TTAAACAAAT | 240 |

GGACAATGTC ATAAATATT TTGAGTTTAT TGAATCTAAA AGTATTGCTT TATATTTTCA 300  
 AAAACGATTA AATGAGCTGA TAGAT 325

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Tyr | Gly | Thr | Phe | Phe | Leu | Gln | Gln | Asn | Arg | Leu | His | Asn | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Lys | Gly | Phe | Thr | His | Tyr | Lys | Tyr | Tyr | Arg | Ala | Glu | Asn | Ser | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ile | Tyr | Ala | Asp | Tyr | Phe | Glu | Met | Lys | Leu | Lys | Lys | Leu | Leu | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Asp | Thr | Lys | Val | Phe | Glu | Lys | Ser | Thr | Phe | Lys | Phe | Val | Glu | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Lys | Ile | Tyr | Leu | Thr | Glu | Ser | Lys | Glu | Ser | Gly | Ile | Lys | Gln | Met |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Asn | Val | Ile | Lys | Tyr | Phe | Glu | Phe | Ile | Glu | Ser | Lys | Ser | Ile | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Tyr | Phe | Gln | Lys | Arg | Leu | Asn | Glu | Leu | Ile | Asp |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 238 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CAACGTTGAG AATTATTTGC GAATGTGTTT GGATAGCATT CAGAATCAGA CGTATCAAAA  | 60  |
| TTTTGAGTGT TTATTAATCA ATGATGGCTC TCCAGATCAT TCATCCAAAA TATGTGAAGA  | 120 |
| ATTTGTAGAG AAAGATTCTC GTTTCAAATA TTTTGAGAAA GCAAACGGCG GTCTTTTCATC | 180 |
| AGCTCGTAAC CTAGGTATTG AATGTTCTGGG GGGGGGCGTA CATTACTTTT GTAGACTC   | 238 |

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 79 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

```

Asn Val Glu Asn Tyr Leu Arg Met Cys Leu Asp Ser Ile Gln Asn Gln
1          5          10          15
Thr Tyr Gln Asn Phe Glu Cys Leu Leu Ile Asn Asp Gly Ser Pro Asp
20          25          30
His Ser Ser Lys Ile Cys Glu Glu Phe Val Glu Lys Asp Ser Arg Phe
35          40          45
Lys Tyr Phe Glu Lys Ala Asn Gly Gly Leu Ser Ser Ala Arg Asn Leu
50          55          60
Gly Ile Glu Cys Ser Gly Gly Gly Val His Tyr Phe Cys Arg Leu
65          70          75

```

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 742 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

```

CTACTATCAA TCAAGTTCTT CAGCCATTGA GGCCACCATT GAGGGCAACA GCCAAACGAC      60
CATCAGCCAG ACTAGCCACT TTATTCAGTC TTATATCAAA AAAC TAGAAA CCACCTCGAC      120
TGGTTTGACC CAGCAGACGG ATGTTCTGGC CTATGCTGAG AATCCCAGTC AAGACAAGGT      180
CGAGGGAATC CGAGATTGTG TTTTGACCAT CTTGAAGTCA GATAAGGACT TGAAAAGTGT      240
TGTGCTGGTG ACCAAATCTG GTCAGGTCAT TTCTACAGAT GACAGTGTGC AGATGAAAAC      300
TTCCTCTGAT ATGATGGCTG AGGATTGGTA CCAAAGGCC ATTCATCAGG GAGCTATGCC      360
TGTTTTGACT CCAGCTCGTA AATCAGATAG TCAGTGGGTC ATTTCTGTCA CTCAAGAACT      420
TGTTGATGCA AAGGGAGCCA ATCTTGGTGT GCTTCGTTTG GATATTTCTT ATGAAACTCT      480
GGAAGCCTAT CTCAATCAAC TCCAGTTGGG GCAGCAGGGC TTTGCCTTCA TTATCAATGA      540
AAACCATGAA TTTGTCTACC ATCCTCAACA CACAGTTTAT AGTTCGTCTA GCAAAATGGA      600
GGCTATGAAA CCCTACATCG ATACAGGTCA GGGTTATACT CCTGGTCACA AATCCTACGT      660
CAGTCAAGAG AAGATTGCAG GAACTGATTG GACGGTGCTT GCGGTGTCAT CATTGGAAAA      720
GTTAGACCAG GTTCGGAGTC AG                                     742

```

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 247 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```

Tyr Tyr Gln Ser Ser Ser Ser Ala Ile Glu Ala Thr Ile Glu Gly Asn
1          5          10          15
Ser Gln Thr Thr Ile Ser Gln Thr Ser His Phe Ile Gln Ser Tyr Ile
          20          25          30
Lys Lys Leu Glu Thr Thr Ser Thr Gly Leu Thr Gln Gln Thr Asp Val
          35          40          45
Leu Ala Tyr Ala Glu Asn Pro Ser Gln Asp Lys Val Glu Gly Ile Arg
          50          55          60
Asp Leu Phe Leu Thr Ile Leu Lys Ser Asp Lys Asp Leu Lys Thr Val
65          70          75          80
Val Leu Val Thr Lys Ser Gly Gln Val Ile Ser Thr Asp Asp Ser Val
          85          90          95
Gln Met Lys Thr Ser Ser Asp Met Met Ala Glu Asp Trp Tyr Gln Lys
          100          105          110
Ala Ile His Gln Gly Ala Met Pro Val Leu Thr Pro Ala Arg Lys Ser
          115          120          125
Asp Ser Gln Trp Val Ile Ser Val Thr Gln Glu Leu Val Asp Ala Lys
          130          135          140
Gly Ala Asn Leu Gly Val Leu Arg Leu Asp Ile Ser Tyr Glu Thr Leu
145          150          155          160
Glu Ala Tyr Leu Asn Gln Leu Gln Leu Gly Gln Gln Gly Phe Ala Phe
          165          170          175
Ile Ile Asn Glu Asn His Glu Phe Val Tyr His Pro Gln His Thr Val
          180          185          190
Tyr Ser Ser Ser Ser Lys Met Glu Ala Met Lys Pro Tyr Ile Asp Thr
          195          200          205
Gly Gln Gly Tyr Thr Pro Gly His Lys Ser Tyr Val Ser Gln Glu Lys
          210          215          220
Ile Ala Gly Thr Asp Trp Thr Val Leu Gly Val Ser Ser Leu Glu Lys
225          230          235          240
Leu Asp Gln Val Arg Ser Gln
          245

```

(2) INFORMATION FOR SEQ ID NO: 171:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GACAAAAACA TTAAACGTC CTGAGGTTTT ATCACCTGCA GGGACTTTAG AGAAGCTAAA   | 60   |
| GGTAGCTGTT CAGTATGGAG CAGATGCTGT CTTTATCGGT GGTCAAGCCT ATGGTCTTCG  | 120  |
| TAGCCGTGCG GGAAACTTTA CTTTCGAACA GATGGAAGAA GGCGTGCAGT TTGCGGCCAA  | 180  |
| GTATGGTGCC AAGGTCTATG TAGCGGCTAA TATGGTTATG CACGAAGGAA ATGAAGCTGG  | 240  |
| TGCTGGTGAG TGGTTCGGTA AACTGCGTGA TATCGGGATT GCAGCAGTTA TCGTATCTGA  | 300  |
| CCCAGCCTTG ATTATGATTG CAGTGACTGA AGCACCAGGC CTTGAAATCC ACCTTTCTAC  | 360  |
| CCAAGCCAGT GCCACTAACT ATGAAACCCT TGAGTTCTGG AAAGAGCTAG GCTTGACTCG  | 420  |
| TGTCGTTTTA GCGCGTGAGG TTTCATGGA AGAATTAGCT GAGATCCGCA AACGTACAGA   | 480  |
| TGTTGAAATT GAAGCCTTTG TCCATGGAGC TATGTGTATT TCATACTCTG GACGTTGTAC  | 540  |
| TCTTTCAAAC CACATGAGTA TGCGTGATGC CAACCGTGGT GGATGTTCTC AGTCATGCCG  | 600  |
| TTGGAAATAC GACCTTTACG ATATGCCATT TGGGAAAGAA CGTAAGAGTT TGCAGGGTGA  | 660  |
| GATTCAGAA GAATTTTCAA TGTCAGCCGT TGACATGTCT ATGATTGACC ANATTCCAGA   | 720  |
| TATGATTGAA AATGGTGTGG ACAGTCTAAA AATCGAAGGA CGTATGNAGT CTATTCACTA  | 780  |
| NGTATCAACA GTAACCAACT GCTACAAGGC GGCTGTGGAT GCCTATCTTG AAAGTCCTGA  | 840  |
| AAAGTTTGAA GCTATCAAAC AAGACTTGGT GGACGAGATG TGGAAGGTTG CCCAACGTGA  | 900  |
| ACTGGCTACA GGATTTTACT ATGGTACACC ATCTGAAAAT GAGCAGTTGT TTGGTGCTCG  | 960  |
| TCGTAAATC CCTGAGTACA AGTTTGTCGC TGAAGTGGTT TCTTATGATG ATGCGGCACA   | 1020 |
| AACAGCAACT ATTCGTCAAC GAAACGTCAT TAACGAAGGG GACCAAGTTG AGTTTTATGG  | 1080 |
| TCCAGGTTTC CGTCATTTTG AAACCTATAT TGAAGATTTG CATGATGCTA AAGGCAATAA  | 1140 |
| AATCGACCGC GCTCCAAATC CAATGGAAC ATTGACTATT AAAGTCCCAC AACCTGTTCA   | 1200 |
| ATCAGGAGAC ATGGTTTCGAG CTCTTAAAGA GGGGCTTATC AATCTTTATA AGGAAGATGG | 1260 |
| AACCAGCGTC ACAGTTCGTG CT                                           | 1282 |

## (2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 427 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Lys | Thr | Leu | Lys | Arg | Pro | Glu | Val | Leu | Ser | Pro | Ala | Gly | Thr | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Glu Lys Leu Lys Val Ala Val Gln Tyr Gly Ala Asp Ala Val Phe Ile  
 20 25 30  
 Gly Gly Gln Ala Tyr Gly Leu Arg Ser Arg Ala Gly Asn Phe Thr Phe  
 35 40 45  
 Glu Gln Met Glu Glu Gly Val Gln Phe Ala Ala Lys Tyr Gly Ala Lys  
 50 55 60  
 Val Tyr Val Ala Ala Asn Met Val Met His Glu Gly Asn Glu Ala Gly  
 65 70 75 80  
 Ala Gly Glu Trp Phe Arg Lys Leu Arg Asp Ile Gly Ile Ala Ala Val  
 85 90 95  
 Ile Val Ser Asp Pro Ala Leu Ile Met Ile Ala Val Thr Glu Ala Pro  
 100 105 110  
 Gly Leu Glu Ile His Leu Ser Thr Gln Ala Ser Ala Thr Asn Tyr Glu  
 115 120 125  
 Thr Leu Glu Phe Trp Lys Glu Leu Gly Leu Thr Arg Val Val Leu Ala  
 130 135 140  
 Arg Glu Val Ser Met Glu Glu Leu Ala Glu Ile Arg Lys Arg Thr Asp  
 145 150 155 160  
 Val Glu Ile Glu Ala Phe Val His Gly Ala Met Cys Ile Ser Tyr Ser  
 165 170 175  
 Gly Arg Cys Thr Leu Ser Asn His Met Ser Met Arg Asp Ala Asn Arg  
 180 185 190  
 Gly Gly Cys Ser Gln Ser Cys Arg Trp Lys Tyr Asp Leu Tyr Asp Met  
 195 200 205  
 Pro Phe Gly Lys Glu Arg Lys Ser Leu Gln Gly Glu Ile Pro Glu Glu  
 210 215 220  
 Phe Ser Met Ser Ala Val Asp Met Ser Met Ile Asp Xaa Ile Pro Asp  
 225 230 235 240  
 Met Ile Glu Asn Gly Val Asp Ser Leu Lys Ile Glu Gly Arg Met Xaa  
 245 250 255  
 Ser Ile His Xaa Val Ser Thr Val Thr Asn Cys Tyr Lys Ala Ala Val  
 260 265 270  
 Asp Ala Tyr Leu Glu Ser Pro Glu Lys Phe Glu Ala Ile Lys Gln Asp  
 275 280 285  
 Leu Val Asp Glu Met Trp Lys Val Ala Gln Arg Glu Leu Ala Thr Gly  
 290 295 300  
 Phe Tyr Tyr Gly Thr Pro Ser Glu Asn Glu Gln Leu Phe Gly Ala Arg  
 305 310 315 320  
 Arg Lys Ile Pro Glu Tyr Lys Phe Val Ala Glu Val Val Ser Tyr Asp  
 325 330 335  
 Asp Ala Ala Gln Thr Ala Thr Ile Arg Gln Arg Asn Val Ile Asn Glu  
 340 345 350

Gly Asp Gln Val Glu Phe Tyr Gly Pro Gly Phe Arg His Phe Glu Thr  
           355                                  360                                  365  
 Tyr Ile Glu Asp Leu His Asp Ala Lys Gly Asn Lys Ile Asp Arg Ala  
           370                                  375                                  380  
 Pro Asn Pro Met Glu Leu Leu Thr Ile Lys Val Pro Gln Pro Val Gln  
           385                                  390                                  395                                  400  
 Ser Gly Asp Met Val Arg Ala Leu Lys Glu Gly Leu Ile Asn Leu Tyr  
                                   405                                  410                                  415  
 Lys Glu Asp Gly Thr Ser Val Thr Val Arg Ala  
                                   420                                  425

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 778 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTCTCAGGAG ACCTTTAAAA ATATCACCAA TAGCTTCTCC ATGCAAATCA ATCGTCGCGT | 60  |
| CAACCAAGGA ACGCCTCGTG GTGCTGGGAA TATCAAGGGT GAAGACATCA AAAAAATCAC | 120 |
| CGAAAACAAG GCCATTGAGT CTTATGTCAA ACGTATCAAC GCTATCGGAG ATTTGACTGG | 180 |
| ATATGACCTG ATTGAAACGC CAGAAACCAA GAAGAATCTC ACTGCTGATC GTGCCAAGCG | 240 |
| TTTTGGAAGT AGCTTGATGA TTACAGGTGT CAATGACTCC TCTAAAGAAG ACAAGTTTGT | 300 |
| CTCTGGTTCT TATAAACTAG TCGAAGGAGA GCACTTAACC AACGACGACA AGGATAAAAT | 360 |
| CCTCTTGCAC AAGGACTTGG CAGCCAAACA CGGCTGGAAA GTAGGGGACA AGGTAAACT  | 420 |
| GGACTCTAAT ATCTACGATG CAGATAATGA AAAAGGAGCC AAGGAAACAG TTGAAGTGAC | 480 |
| AATCAAGGGA CTCTTTGATG GTCATAATAA GTCAGCAGTA ACCTACTCAC AAGAACTTTA | 540 |
| CGAAAACACA GCTATTACAG ACATTCACAC TGCTGCAAAA CTTTATGGAT ACACAGAAGA | 600 |
| CACAGCCATT TATGGGGACG CAACCTTCTT TGTAACAGCA GACAAGAACT TGGATGATGT | 660 |
| TATGAAAGAG TTGAATGGCA TCAGTGGTAT CAACTGGAAG AGCTACACAC TCGTCAAGAG | 720 |
| CTCCTCTAAC TACCCAGCTC TTGAGCAATC TATCTCTGGT ATGTACAAGA TGGCCAAC   | 778 |

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 259 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ser Gln Glu Thr Phe Lys Asn Ile Thr Asn Ser Phe Ser Met Gln Ile  
 1 5 10 15  
 Asn Arg Arg Val Asn Gln Gly Thr Pro Arg Gly Ala Gly Asn Ile Lys  
 20 25 30  
 Gly Glu Asp Ile Lys Lys Ile Thr Glu Asn Lys Ala Ile Glu Ser Tyr  
 35 40 45  
 Val Lys Arg Ile Asn Ala Ile Gly Asp Leu Thr Gly Tyr Asp Leu Ile  
 50 55 60  
 Glu Thr Pro Glu Thr Lys Lys Asn Leu Thr Ala Asp Arg Ala Lys Arg  
 65 70 75 80  
 Phe Gly Ser Ser Leu Met Ile Thr Gly Val Asn Asp Ser Ser Lys Glu  
 85 90 95  
 Asp Lys Phe Val Ser Gly Ser Tyr Lys Leu Val Glu Gly Glu His Leu  
 100 105 110  
 Thr Asn Asp Asp Lys Asp Lys Ile Leu Leu His Lys Asp Leu Ala Ala  
 115 120 125  
 Lys His Gly Trp Lys Val Gly Asp Lys Val Lys Leu Asp Ser Asn Ile  
 130 135 140  
 Tyr Asp Ala Asp Asn Glu Lys Gly Ala Lys Glu Thr Val Glu Val Thr  
 145 150 155 160  
 Ile Lys Gly Leu Phe Asp Gly His Asn Lys Ser Ala Val Thr Tyr Ser  
 165 170 175  
 Gln Glu Leu Tyr Glu Asn Thr Ala Ile Thr Asp Ile His Thr Ala Ala  
 180 185 190  
 Lys Leu Tyr Gly Tyr Thr Glu Asp Thr Ala Ile Tyr Gly Asp Ala Thr  
 195 200 205  
 Phe Phe Val Thr Ala Asp Lys Asn Leu Asp Asp Val Met Lys Glu Leu  
 210 215 220  
 Asn Gly Ile Ser Gly Ile Asn Trp Lys Ser Tyr Thr Leu Val Lys Ser  
 225 230 235 240  
 Ser Ser Asn Tyr Pro Ala Leu Glu Gln Ser Ile Ser Gly Met Tyr Lys  
 245 250 255  
 Met Ala Asn

## (2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 694 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

```

AGTAAATGCG CAATCAAATT CATTAATATT AATAGATGAA CCTGAAATCT CACTTCATCC      60
GAGTGCAATC TATAAATTTA AAGAGTTTTT ACTTCAAGAG TGTTTAAATA AAAAACATCA      120
AATTATTATC ACTACACATT CTACACAACT TATAAAAGAT TTTCCTAGAG AAGCCGTGAA      180
ACTTTTAGTG AAAAACGGAG AAAAGGTAGA TGTTATTGAA AATATTGATT ATCAGGATGC      240
ATTTTTTGAA TTAGGTGATG TGTATCATTC TAGGAAGATG ATTTATGTTG AAGATAGACT      300
AGCTAAATAT ATTCTAGAGT TTGTTATCAC TCATTGAGGT AGTGAGAATC TTAAACAGAA      360
TTTAGTAGTG AGATATATTC CTGGTGGAGC AAATCAAATA ATTTGTAATA ATATTTTAAA      420
CTCATCGTAT TTAGATTCCG ATAACCATTA TTTTGGCTT GATGGAGATC AAAACACTAA      480
TGTTAGTGAA TCAAATAATT TAATGAACTA TCTTGAAAAT GGTGTTGTTA TATCAGATAA      540
AATTCCTGAA TCAGATAATA AAAATCTTGA TGATATTATA AAATTGATAA NGGGATGTCC      600
AATTAAATTT AATGTTTCAG GTAATAAAGG GCAAAAAAAT AATATTGAAT TAATTGCGAA      660
ACAAAGAAGC TTTATAGATT ATTGGGCTAA ATAC      694

```

## (2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 231 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```

Val Asn Ala Gln Ser Asn Ser Leu Ile Leu Ile Asp Glu Pro Glu Ile
1          5          10          15
Ser Leu His Pro Ser Ala Ile Tyr Lys Phe Lys Glu Phe Leu Leu Gln
20        25        30
Glu Cys Leu Asn Lys Lys His Gln Ile Ile Ile Thr Thr His Ser Thr
35        40        45
Gln Leu Ile Lys Asp Phe Pro Arg Glu Ala Val Lys Leu Leu Val Lys
50        55        60
Asn Gly Glu Lys Val Asp Val Ile Glu Asn Ile Asp Tyr Gln Asp Ala
65        70        75        80
Phe Phe Glu Leu Gly Asp Val Tyr His Ser Arg Lys Met Ile Tyr Val
85        90        95
Glu Asp Arg Leu Ala Lys Tyr Ile Leu Glu Phe Val Ile Thr His Ser
100       105       110
Gly Ser Glu Asn Leu Lys Gln Asn Leu Val Val Arg Tyr Ile Pro Gly
115       120       125
Gly Ala Asn Gln Ile Ile Cys Asn Asn Ile Leu Asn Ser Ser Tyr Leu
130       135       140

```

Asp Ser Asp Asn His Tyr Phe Trp Leu Asp Gly Asp Gln Asn Thr Asn  
 145 150 155 160  
 Val Ser Glu Ser Asn Asn Leu Met Asn Tyr Leu Glu Asn Gly Val Val  
 165 170 175  
 Ile Ser Asp Lys Ile Pro Glu Ser Asp Asn Lys Asn Leu Asp Asp Ile  
 180 185 190  
 Ile Lys Leu Ile Xaa Gly Cys Pro Ile Lys Phe Asn Val Ser Gly Asn  
 195 200 205  
 Lys Gly Gln Lys Asn Asn Ile Glu Leu Ile Ala Lys Gln Arg Ser Phe  
 210 215 220  
 Ile Asp Tyr Trp Ala Lys Tyr  
 225 230

## (2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 550 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTACCGCGTT CATCAAGATG TCAAACAAGT CATGACCTAT CAACCCATGG TGCGAGAAAT  | 60  |
| ATTGAGTGAA CAAGACACCC CAGCAAACGA AGAGCTTGTG CTTGCTATGA TTTATACTGA  | 120 |
| AACAAAAGGA AAAGAAGGCG ATGTTATGCA GTCTAGTGAG TCTGCAAGTG GTTCCACCAA  | 180 |
| CACCATCAAT GATAATGCCT CTAGCATTCTG GCAAGGCATT CAAACTCTGA CAGGCAATCT | 240 |
| CTATCTGGCG CAGAAGAAGG GGGTAGATAT CTGGACAGCT GTTCAAGCCT ATAATTTTGG  | 300 |
| ACCTGCCTAT ATCGATTTTA TCGCCCAAAA TGGCAAGGAA AATACCCCTGG CTCTAGCCAA | 360 |
| ACAGTACTCT CGTGAGACTG TTGCCCCCTT GCTTGGTAAT AGGACTGGAA AGACTTATAG  | 420 |
| TTATATTACAC CCCATTTCCA TTTTTCACGG TGCTGAACTC TATGTAAATG GAGGAAACTA | 480 |
| TTATTATTCT AGACAGGTAC GACTTAACCT TTACATCATC AAATGTTTCA CTCTCTTTTC  | 540 |
| AACATCTGGC                                                         | 550 |

## (2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 183 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Tyr Arg Val His Gln Asp Val Lys Gln Val Met Thr Tyr Gln Pro Met  
 1 5 10 15  
 Val Arg Glu Ile Leu Ser Glu Gln Asp Thr Pro Ala Asn Glu Glu Leu  
 20 25 30  
 Val Leu Ala Met Ile Tyr Thr Glu Thr Lys Gly Lys Glu Gly Asp Val  
 35 40 45  
 Met Gln Ser Ser Glu Ser Ala Ser Gly Ser Thr Asn Thr Ile Asn Asp  
 50 55 60  
 Asn Ala Ser Ser Ile Arg Gln Gly Ile Gln Thr Leu Thr Gly Asn Leu  
 65 70 75 80  
 Tyr Leu Ala Gln Lys Lys Gly Val Asp Ile Trp Thr Ala Val Gln Ala  
 85 90 95  
 Tyr Asn Phe Gly Pro Ala Tyr Ile Asp Phe Ile Ala Gln Asn Gly Lys  
 100 105 110  
 Glu Asn Thr Leu Ala Leu Ala Lys Gln Tyr Ser Arg Glu Thr Val Ala  
 115 120 125  
 Pro Leu Leu Gly Asn Arg Thr Gly Lys Thr Tyr Ser Tyr Ile His Pro  
 130 135 140  
 Ile Ser Ile Phe His Gly Ala Glu Leu Tyr Val Asn Gly Gly Asn Tyr  
 145 150 155 160  
 Tyr Tyr Ser Arg Gln Val Arg Leu Asn Leu Tyr Ile Ile Lys Cys Phe  
 165 170 175  
 Thr Leu Phe Ser Thr Ser Gly  
 180

## (2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GTGGATGGGC TTAACTATC TTCGTATTCG CCGTGCGGCT AAAATTGTGG ACAATGAGGA 60  
 GTTTGAAGCC TTGATTCGTA CGGGTCAATT GATTGATTG CGCGACCCAG CAGAATTCCA 120  
 CAGAAAACAT ATCCTTGGTG CACGCAATAT TCCTTCAAGT CAGTTGAAAA CTAGTCTTGC 180  
 AGCCCTTCGT AAAGATAAAC CTGTCCCTCT CTACGAAAAC CAACGTGCGC AACGAGTTAC 240  
 AAATGCAGCT CTTTACTTGA AAAAACAAGG TTTTCTGAG ATTTATATCC TTTCTTATGG 300  
 CTTGGATTCT TGGAAAGGGA AAGTGAAGAC TAGC 334

## (2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 amino acids

- (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```

Trp Met Gly Phe Asn Tyr Leu Arg Ile Arg Arg Ala Ala Lys Ile Val
1          5          10          15
Asp Asn Glu Glu Phe Glu Ala Leu Ile Arg Thr Gly Gln Leu Ile Asp
20          25          30
Leu Arg Asp Pro Ala Glu Phe His Arg Lys His Ile Leu Gly Ala Arg
35          40          45
Asn Ile Pro Ser Ser Gln Leu Lys Thr Ser Leu Ala Ala Leu Arg Lys
50          55          60
Asp Lys Pro Val Leu Leu Tyr Glu Asn Gln Arg Ala Gln Arg Val Thr
65          70          75          80
Asn Ala Ala Leu Tyr Leu Lys Lys Gln Gly Phe Ser Glu Ile Tyr Ile
85          90          95
Leu Ser Tyr Gly Leu Asp Ser Trp Lys Gly Lys Val Lys Thr Ser
100          105          110

```

(2) INFORMATION FOR SEQ ID NO: 181:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

```

ACTAACCAG CATCGTTCGC AGGAAAATAA GGACAATAAT CGTGTCTCTT ATGTGGATGG      60
CAGCCAGTCA AGTCAGAAAA GTGAAAACCTT GACACCAGAC CAGGTTAGCC AGAAAGAAGG      120
AATTCAGGCT GAGCAAATTG TAATCAAAAT TACAGATCAG GGCTATGTAA CGTCACACGG      180
TGACCACTAT CATTACTATA ATGGGAAAGT TCCTTATGAT GCCCTCTTTA GTGAAGAACT      240
CTTGATGAAG GATCCAAACT ATCAACTTAA AGACGCTGAT ATTGTCAATG AAGTCAAGGG      300
TGGTTATATC ATCAAGGTCG ATGGAAAATA TTATGTCTAC CTGAAAGATG CAGCTCATGC      360
TGATAATGTT CGAACTAAAG ATGAAATCAA TCGTCAAAAA CAAGAACATG TCAAAGATAA      420
TGAGAAGGTT AACTCTAATG TTGCTGTAGC AAGGTCTCAG GGACGATATA CGACAAATGA      480
TGGTTATGTC TTTAATCCAG CTGATATTAT CGAAGATACG GGTAATGCTT ATATCGTTCC      540
TCATGGAGGT CACTATCACT ACATTCCCAA AAGCGATTTA TCTGCTAGTG AATTAGCAGC      600
AGCTAAAGCA CATCTGGCTG GAAAAAATAT GCAACCGAGT CAGTTAAGCT ATTCTTCAAC      660

```

```

AGCTAGTGAC AATAACACGC AATCTGTAGC AAAAGGATCA ACTAGCAAGC CAGCAAATAA      720
ATCTGAAAAT CTCCAGAGTC TTTTGAAGGA ACTCTATGAT TCACCTAGCG CCCAACGTTA      780
CAGTGAATCA GATGGCCTGG TCTTTGACCC TGCTAAGATT ATCAGTCGTA CACCAAATGG      840
AGTTGCGATT CCGCATGGCG ACCATTACCA CTTTATTCCCT TACAGCAAGC TTTCTGCCTT      900
AGAAGAAAAG ATTGCCAGAA TGGTGCCTAT CAGTGGAAC TGGTCTACAG TTTCTACAAA      960
TGCAAAACCT AATGAAGTAG TGTCTAGTCT AGGCAGTCTT TCAAGCAATC CTTCTTCTTT     1020
AACGACAAGT AAGGAGCTCT CTTCAGCATC TGATGGTTAT ATTTTAAATC CAAAAGATAT     1080
CGTTGAAGAA ACGGCTACAG CTTATATTGT AAGACATGGT GATCATTTCC ATTACATTCC     1140
AAAATCAAAT CAAATTGGGC AACCGACTCT TCCAAACAAT AGTCTAGCAA CACCTTCTCC     1200
ATCTCTTCCA ATCAATCCAG GAACTTCACA TGAGAAACAT GAAGAAGATG GATACGGATT     1260
TGATGCTAAT CGTATTATCG CTGAAGATGA ATCAGGTTTT GTCATGAGTC ACGGAGACCA     1320
CAATCATTAT TTCTTCAAGA AG   1342

```

## (2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 447 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

```

Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn Asn Arg Val Ser
1          5          10          15
Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu Asn Leu Thr Pro
20        25        30
Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu Gln Ile Val Ile
35        40        45
Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly Asp His Tyr His
50        55        60
Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe Ser Glu Glu Leu
65        70        75        80
Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala Asp Ile Val Asn
85        90        95
Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly Lys Tyr Tyr Val
100       105       110
Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg Thr Lys Asp Glu
115       120       125
Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn Glu Lys Val Asn
130       135       140

```

Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr Thr Thr Asn Asp  
 145 150 155 160  
 Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp Thr Gly Asn Ala  
 165 170 175  
 Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile Pro Lys Ser Asp  
 180 185 190  
 Leu Ser Ala Ser Glu Leu Ala Ala Ala Lys Ala His Leu Ala Gly Lys  
 195 200 205  
 Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr Ala Ser Asp Asn  
 210 215 220  
 Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys Pro Ala Asn Lys  
 225 230 235 240  
 Ser Glu Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr Asp Ser Pro Ser  
 245 250 255  
 Ala Gln Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe Asp Pro Ala Lys  
 260 265 270  
 Ile Ile Ser Arg Thr Pro Asn Gly Val Ala Ile Pro His Gly Asp His  
 275 280 285  
 Tyr His Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu Glu Glu Lys Ile  
 290 295 300  
 Ala Arg Met Val Pro Ile Ser Gly Thr Gly Ser Thr Val Ser Thr Asn  
 305 310 315 320  
 Ala Lys Pro Asn Glu Val Val Ser Ser Leu Gly Ser Leu Ser Ser Asn  
 325 330 335  
 Pro Ser Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser Ala Ser Asp Gly  
 340 345 350  
 Tyr Ile Phe Asn Pro Lys Asp Ile Val Glu Glu Thr Ala Thr Ala Tyr  
 355 360 365  
 Ile Val Arg His Gly Asp His Phe His Tyr Ile Pro Lys Ser Asn Gln  
 370 375 380  
 Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro Ser Pro  
 385 390 395 400  
 Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu Glu Asp  
 405 410 415  
 Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu Ser Gly  
 420 425 430  
 Phe Val Met Ser His Gly Asp His Asn His Tyr Phe Phe Lys Lys  
 435 440 445

## (2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 934 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TGACTACCTT GAAATCCCAC TTTACAGCTA TCTTGGTGGG TTCAACACTA AAGTTCTTCC  | 60  |
| AACTCCAATG ATGAACATCA TCAACGGTGG TTCTCACTCT GACGCTCCAA TCGCTTTCCA  | 120 |
| AGAGTTCATG ATCTTGCCAG TTGGTGCGCC AACATTTAAA GAAGCCCTTC GTTACGGTGC  | 180 |
| TGAAATCTTC CACGCTCTTA AGAAAATCCT TAAATCACGT GGTTTGGAAA CTGCCGTAGG  | 240 |
| TGACGAAGGT GGATTGCTC CTCGTTTCGA AGGAACTGAA GATGGTGTTG AAACATATCCT  | 300 |
| TGCTGCGATT GAAGCTGCTG GATATGTACC AGGTAAAGAC GTATTTATCG GATTTGACTG  | 360 |
| TGCTTCATCA GAATTCTACG ATAAAGAACG TAAAGTTTAC GACTACACTA AATTTGAAGG  | 420 |
| TGAAGGTGCT GCTGTTTCGTA CATCTGCAGA ACAAATCGAC TACCTTGAAG AATTGGTTAA | 480 |
| CAAATACCCA ATCATCACTA TTGAAGATGG TATGGATGAA AACGACTGGG ATGGTTGGAA  | 540 |
| AGCTCTTACT GAACGTCTTG GTAAGAAAGT ACAACTTGTT GGTGACGACT TCTTCGTAAC  | 600 |
| AAACACTGAC TACCTTGACG GTGGTATCCA AGAAGGTGCT GCTAACTCAA TCCTTATCAA  | 660 |
| AGTTAACCAA ATCGGTACTC TTAAGTAAAC TTTTGAAGCT ATCGAAATGG CTAAAGAAGC  | 720 |
| TGGTTACACT GCTGTTGTAT CACACCGTTC AGGTGAAACT GAAGATTCAA CAATCGCTGA  | 780 |
| TATTGCAGTT GCAACTAACG CAGGACAAAT CAAGACTGGT TCACTTTCAC GTACAGACCG  | 840 |
| CATCGCTAAA TACAACCAAT TGCTTCGTAT CGAAGACCAA CTTGGTGAAG TAGCTGAATA  | 900 |
| TCGTGGATTG AAATCAATTCT ACAACCTTAA AAAA                             | 934 |

## (2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 311 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Tyr | Leu | Glu | Ile | Pro | Leu | Tyr | Ser | Tyr | Leu | Gly | Gly | Phe | Asn | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Val | Leu | Pro | Thr | Pro | Met | Met | Asn | Ile | Ile | Asn | Gly | Gly | Ser | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Asp | Ala | Pro | Ile | Ala | Phe | Gln | Glu | Phe | Met | Ile | Leu | Pro | Val | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Pro | Thr | Phe | Lys | Glu | Ala | Leu | Arg | Tyr | Gly | Ala | Glu | Ile | Phe | His |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Leu | Lys | Lys | Ile | Leu | Lys | Ser | Arg | Gly | Leu | Glu | Thr | Ala | Val | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

Asp Glu Gly Gly Phe Ala Pro Arg Phe Glu Gly Thr Glu Asp Gly Val  
 85 90 95  
 Glu Thr Ile Leu Ala Ala Ile Glu Ala Ala Gly Tyr Val Pro Gly Lys  
 100 105 110  
 Asp Val Phe Ile Gly Phe Asp Cys Ala Ser Ser Glu Phe Tyr Asp Lys  
 115 120 125  
 Glu Arg Lys Val Tyr Asp Tyr Thr Lys Phe Glu Gly Glu Gly Ala Ala  
 130 135 140  
 Val Arg Thr Ser Ala Glu Gln Ile Asp Tyr Leu Glu Glu Leu Val Asn  
 145 150 155 160  
 Lys Tyr Pro Ile Ile Thr Ile Glu Asp Gly Met Asp Glu Asn Asp Trp  
 165 170 175  
 Asp Gly Trp Lys Ala Leu Thr Glu Arg Leu Gly Lys Lys Val Gln Leu  
 180 185 190  
 Val Gly Asp Asp Phe Phe Val Thr Asn Thr Asp Tyr Leu Ala Arg Gly  
 195 200 205  
 Ile Gln Glu Gly Ala Ala Asn Ser Ile Leu Ile Lys Val Asn Gln Ile  
 210 215 220  
 Gly Thr Leu Thr Glu Thr Phe Glu Ala Ile Glu Met Ala Lys Glu Ala  
 225 230 235 240  
 Gly Tyr Thr Ala Val Val Ser His Arg Ser Gly Glu Thr Glu Asp Ser  
 245 250 255  
 Thr Ile Ala Asp Ile Ala Val Ala Thr Asn Ala Gly Gln Ile Lys Thr  
 260 265 270  
 Gly Ser Leu Ser Arg Thr Asp Arg Ile Ala Lys Tyr Asn Gln Leu Leu  
 275 280 285  
 Arg Ile Glu Asp Gln Leu Gly Glu Val Ala Glu Tyr Arg Gly Leu Lys  
 290 295 300  
 Ser Phe Tyr Asn Leu Lys Lys  
 305 310

(2) INFORMATION FOR SEQ ID NO: 185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 541 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TCGTATCTTT TTTTGGAGCA ATGTTGCGGT AGAAGGACAT TCCATGGATC CGACCCTAGC  | 60  |
| GGATGGCGGAA ATTCTCTTCG TTGTAAAACA CCTTCCTATT GACCGTTTTG ATATCGTGGT | 120 |
| GGCCCCATGAG GAAGATGGCA ATAAGGACAT CGTCAAGCGC GTGATTGGAA TGCCTGGCGA | 180 |

CACCATTTCGT TACGAAAATG ATAAACTCTA CATCAATGAC AAAGAAACGG ACGAGCCTTA 240  
 TCTAGCAGAC TATATCAAAC GCTTCAAGGA TGACAACTC CAAAGCACTT ACTCAGGCAA 300  
 GGGCTTTGAA GGAAATAAAG GAACTTTCTT TAGAAGTATC GCTCAAAAAG CTCAAGCCTT 360  
 CACAGTTGAT GTCAACTACA ACACCAACTT TAGCTTTACT GTTCCAGAAG GAGAATACCT 420  
 TCTCCTCGGA GATGACCGCT TGGTTTCGAG CGACAGCCGC CACGTAGGTA CCTTCAAAGC 480  
 AAAAGATATC ACAGGGGAAG CTAAATTCCG CTTATGGCEA ATCACCCGTA TCGGAACATT 540  
 T 541

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ile | Phe | Phe | Trp | Ser | Asn | Val | Arg | Val | Glu | Gly | His | Ser | Met | Asp | 1   | 5   | 10  | 15  |
| Pro | Thr | Leu | Ala | Asp | Gly | Glu | Ile | Leu | Phe | Val | Val | Lys | His | Leu | Pro | 20  | 25  | 30  |     |
| Ile | Asp | Arg | Phe | Asp | Ile | Val | Val | Ala | His | Glu | Glu | Asp | Gly | Asn | Lys | 35  | 40  | 45  |     |
| Asp | Ile | Val | Lys | Arg | Val | Ile | Gly | Met | Pro | Gly | Asp | Thr | Ile | Arg | Tyr | 50  | 55  | 60  |     |
| Glu | Asn | Asp | Lys | Leu | Tyr | Ile | Asn | Asp | Lys | Glu | Thr | Asp | Glu | Pro | Tyr | 65  | 70  | 75  | 80  |
| Leu | Ala | Asp | Tyr | Ile | Lys | Arg | Phe | Lys | Asp | Asp | Lys | Leu | Gln | Ser | Thr | 85  | 90  | 95  |     |
| Tyr | Ser | Gly | Lys | Gly | Phe | Glu | Gly | Asn | Lys | Gly | Thr | Phe | Phe | Arg | Ser | 100 | 105 | 110 |     |
| Ile | Ala | Gln | Lys | Ala | Gln | Ala | Phe | Thr | Val | Asp | Val | Asn | Tyr | Asn | Thr | 115 | 120 | 125 |     |
| Asn | Phe | Ser | Phe | Thr | Val | Pro | Glu | Gly | Glu | Tyr | Leu | Leu | Leu | Gly | Asp | 130 | 135 | 140 |     |
| Asp | Arg | Leu | Val | Ser | Ser | Asp | Ser | Arg | His | Val | Gly | Thr | Phe | Lys | Ala | 145 | 150 | 155 | 160 |
| Lys | Asp | Ile | Thr | Gly | Glu | Ala | Lys | Phe | Arg | Leu | Trp | Pro | Ile | Thr | Arg | 165 | 170 | 175 |     |
| Ile | Gly | Thr | Phe |     |     |     |     |     |     |     |     |     |     |     |     | 180 |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGACTCTCTC AAAGATGTGA AAGCAAATGC TAGCGACAGC AAGCCTGCAC AGGACAAGAA | 60  |
| GGATGCAAAA CAAGGAACGG AAGATAGTAA GGATTCAGAT AAGATGACTG AAACAAACTC | 120 |
| AGTTCCGGCA GGAGTGATTG TGGTCAGTCT ACTTGCCCTC CTAGGCGTGA TTGCCTTCTG | 180 |
| GCTGATTTCG CGTAAGAAAG AGTCAGAAAT CCAGCAATTA AGCACGGAAT TGATCAAGGT | 240 |
| TCTAGGACAG CTAGATGCAG AAAAAGCGGA TAAAAAGTC CTTGCCAAAG CCCAAAACCT  | 300 |
| TCTCCAAGAA ACCCTTGATT TCGTGAAAGA AGAAAATGGC TCAGCAGAGA CAGAAACTAA | 360 |
| ACTAGTAGAG GAGCTTAAAG CAATCCTTGA CAAACTCAAG                       | 400 |

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 133 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

|                                                                 |     |     |     |    |
|-----------------------------------------------------------------|-----|-----|-----|----|
| Asp Ser Leu Lys Asp Val Lys Ala Asn Ala Ser Asp Ser Lys Pro Ala | 1   | 5   | 10  | 15 |
| Gln Asp Lys Lys Asp Ala Lys Gln Gly Thr Glu Asp Ser Lys Asp Ser | 20  | 25  | 30  |    |
| Asp Lys Met Thr Glu Thr Asn Ser Val Pro Ala Gly Val Ile Val Val | 35  | 40  | 45  |    |
| Ser Leu Leu Ala Leu Leu Gly Val Ile Ala Phe Trp Leu Ile Arg Arg | 50  | 55  | 60  |    |
| Lys Lys Glu Ser Glu Ile Gln Gln Leu Ser Thr Glu Leu Ile Lys Val | 65  | 70  | 75  | 80 |
| Leu Gly Gln Leu Asp Ala Glu Lys Ala Asp Lys Lys Val Leu Ala Lys | 85  | 90  | 95  |    |
| Ala Gln Asn Leu Leu Gln Glu Thr Leu Asp Phe Val Lys Glu Glu Asn | 100 | 105 | 110 |    |
| Gly Ser Ala Glu Thr Glu Thr Lys Leu Val Glu Glu Leu Lys Ala Ile | 115 | 120 | 125 |    |
| Leu Asp Lys Leu Lys                                             | 130 |     |     |    |

## (2) INFORMATION FOR SEQ ID NO: 189:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1201 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

|                                                                     |      |
|---------------------------------------------------------------------|------|
| CAAGAAATCC TATCATCTCT TCCAGAAGCA AACAGAGACG AGGGGAATTC AGACTCAGTT   | 60   |
| GATTGAAGAA TCGCTTAGTC AGCAGACTAT AATCCAGTCC TTCAATGCTC AAACAGAATT   | 120  |
| TATCCAAAGA TTGCGTGAGG CTCATGACAA CTA CT CAGGC TATTCTCAGT CAGCCATCTT | 180  |
| TTATTCTTCA ACGGTCAATC CTTCGACTCG CTTTGTAAAT GCACTCATTT ATGCCCTTTT   | 240  |
| AGCTGGAGTA GGAGCTTATC GTATCATGAT GGGTTCAGCC TTGACCGTCG GTCGTTTAGT   | 300  |
| GACTTTTTTTG AACTATGTTT AGCAATACAC CAAGCCCTTT AACGATATTT CTTCAGTGCT  | 360  |
| AGCTGAGTTG CAAAGTGCTC TGGCTTGCGT AGAGCGTATC TATGGAGTCT TAGATAGCCC   | 420  |
| TGAAGTGGCT GAAACAGGTA AGGAAGTCTT GACGACCAGT GACCAAGTTA AGGGAGCTAT   | 480  |
| TTCTTTTAAA CATGTCTCTT TTGGCTACCA TCCTGAAAAA ATTTTGATTA AGGACTTGTC   | 540  |
| TATCGATATT CCAGCTGGTA GTAAGGTAGC CATCGTTGGT CCGACAGGTG CTGGAATATC   | 600  |
| AACTCTTATC AATCTCCTTA TGCCTTTTTT TCCCATTAGC TCGGGAGATA TCTTGCTGGA   | 660  |
| TGGGCAATCC ATTTATGATT ATACACGAGT ATCATTGAGA CAGCAGTTTG GTATGGTGCT   | 720  |
| TCAAGAAACC TGGCTCACAC AAGGGACCAT TCATGATAAT ATTGCCTTTG GCAATCCTGA   | 780  |
| AGCCAGTCGA GAGCAAGTAA TTGCTGCTGC CAAAGCAGCT AATGCAGACT TTTTCATCCA   | 840  |
| ACAGTTGCCA CAGGGATACG ATACCAAGTT GGAAAATGCT GGAGAATCTC TCTCTGTCGG   | 900  |
| CCAAGCTCAG CTCTTGACCA TAGCCCGAGT CTTTCTGGCT ATTCCAAAGA TTCTTATCTT   | 960  |
| AGACGAGGCA ACTTCTTCCA TTGATACACG GACAGAAGTG CTGGTACAGG ATGCCTTTGC   | 1020 |
| AAAACATCATG AAGGGCCGCA CAAGTTTCAT CATTGCTCAC CGTTTGTCAT CCATTCAGGA  | 1080 |
| TGCGGATTTA ATTCTTGCTT TAGTAGATGG TGATATTGTT GAATATGGTA ACCATCAAGA   | 1140 |
| ACTCATGGAT AGAAAGGGTA AGTATTACCA AATGCAAAAA GCTGCGGCTT TTAGTTCTGA   | 1200 |
| A                                                                   | 1201 |

## (2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Ser | Tyr | His | Leu | Phe | Gln | Lys | Gln | Thr | Glu | Thr | Arg | Gly | Ile | 1   | 5   | 10  | 15  |
| Gln | Thr | Gln | Leu | Ile | Glu | Glu | Ser | Leu | Ser | Gln | Gln | Thr | Ile | Ile | Gln | 20  | 25  | 30  |     |
| Ser | Phe | Asn | Ala | Gln | Thr | Glu | Phe | Ile | Gln | Arg | Leu | Arg | Glu | Ala | His | 35  | 40  | 45  |     |
| Asp | Asn | Tyr | Ser | Gly | Tyr | Ser | Gln | Ser | Ala | Ile | Phe | Tyr | Ser | Ser | Thr | 50  | 55  | 60  |     |
| Val | Asn | Pro | Ser | Thr | Arg | Phe | Val | Asn | Ala | Leu | Ile | Tyr | Ala | Leu | Leu | 65  | 70  | 75  | 80  |
| Ala | Gly | Val | Gly | Ala | Tyr | Arg | Ile | Met | Met | Gly | Ser | Ala | Leu | Thr | Val | 85  | 90  | 95  |     |
| Gly | Arg | Leu | Val | Thr | Phe | Leu | Asn | Tyr | Val | Gln | Gln | Tyr | Thr | Lys | Pro | 100 | 105 | 110 |     |
| Phe | Asn | Asp | Ile | Ser | Ser | Val | Leu | Ala | Glu | Leu | Gln | Ser | Ala | Leu | Ala | 115 | 120 | 125 |     |
| Cys | Val | Glu | Arg | Ile | Tyr | Gly | Val | Leu | Asp | Ser | Pro | Glu | Val | Ala | Glu | 130 | 135 | 140 |     |
| Thr | Gly | Lys | Glu | Val | Leu | Thr | Thr | Ser | Asp | Gln | Val | Lys | Gly | Ala | Ile | 145 | 150 | 155 | 160 |
| Ser | Phe | Lys | His | Val | Ser | Phe | Gly | Tyr | His | Pro | Glu | Lys | Ile | Leu | Ile | 165 | 170 | 175 |     |
| Lys | Asp | Leu | Ser | Ile | Asp | Ile | Pro | Ala | Gly | Ser | Lys | Val | Ala | Ile | Val | 180 | 185 | 190 |     |
| Gly | Pro | Thr | Gly | Ala | Gly | Lys | Ser | Thr | Leu | Ile | Asn | Leu | Leu | Met | Arg | 195 | 200 | 205 |     |
| Phe | Tyr | Pro | Ile | Ser | Ser | Gly | Asp | Ile | Leu | Leu | Asp | Gly | Gln | Ser | Ile | 210 | 215 | 220 |     |
| Tyr | Asp | Tyr | Thr | Arg | Val | Ser | Leu | Arg | Gln | Gln | Phe | Gly | Met | Val | Leu | 225 | 230 | 235 | 240 |
| Gln | Glu | Thr | Trp | Leu | Thr | Gln | Gly | Thr | Ile | His | Asp | Asn | Ile | Ala | Phe | 245 | 250 | 255 |     |
| Gly | Asn | Pro | Glu | Ala | Ser | Arg | Glu | Gln | Val | Ile | Ala | Ala | Ala | Lys | Ala | 260 | 265 | 270 |     |
| Ala | Asn | Ala | Asp | Phe | Phe | Ile | Gln | Gln | Leu | Pro | Gln | Gly | Tyr | Asp | Thr | 275 | 280 | 285 |     |
| Lys | Leu | Glu | Asn | Ala | Gly | Glu | Ser | Leu | Ser | Val | Gly | Gln | Ala | Gln | Leu | 290 | 295 | 300 |     |
| Leu | Thr | Ile | Ala | Arg | Val | Phe | Leu | Ala | Ile | Pro | Lys | Ile | Leu | Ile | Leu | 305 | 310 | 315 | 320 |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Asp        | Glu        | Ala        | Thr        | Ser<br>325 | Ser        | Ile        | Asp        | Thr        | Arg<br>330 | Thr        | Glu        | Val        | Leu        | Val<br>335 | Gln        |
| Asp        | Ala        | Phe        | Ala<br>340 | Lys        | Leu        | Met        | Lys        | Gly<br>345 | Arg        | Thr        | Ser        | Phe        | Ile<br>350 | Ile        | Ala        |
| His        | Arg        | Leu<br>355 | Ser        | Thr        | Ile        | Gln        | Asp<br>360 | Ala        | Asp        | Leu        | Ile        | Leu<br>365 | Val        | Leu        | Val        |
| Asp        | Gly<br>370 | Asp        | Ile        | Val        | Glu        | Tyr<br>375 | Gly        | Asn        | His        | Gln        | Glu<br>380 | Leu        | Met        | Asp        | Arg        |
| Lys<br>385 | Gly        | Lys        | Tyr        | Tyr        | Gln<br>390 | Met        | Gln        | Lys        | Ala        | Ala<br>395 | Ala        | Phe        | Ser        | Ser        | Glu<br>400 |

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1033 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

|            |            |            |            |             |            |      |
|------------|------------|------------|------------|-------------|------------|------|
| ACGAAATGCA | GGGCAGACAG | ATGCCTCGCA | AATTGAAAAG | GCGGCAGTTA  | GCCAAGGAGG | 60   |
| AAAAGCAGTG | AAAAAACAG  | AAATTAGTAA | AGACGCAGAC | TTGCACGAAA  | TTTATCTAGC | 120  |
| TGGAGGTTGT | TTCTGGGGAG | TGGAGGAATA | TTTCTCACGT | GTTCCCGGGG  | TGACGGATGC | 180  |
| CGTTTCAGGC | TATGCAAATG | GTAGAGGAGA | AACAACCAAG | TACGAATTGA  | TTAACCAAAC | 240  |
| AGGTCATGCA | GAAACCGTCC | ATGTCACCTA | TGATGCCAAG | CAAATTTCTC  | TCAAGGAAAT | 300  |
| CCTGCTTCAC | TATTTCCGCA | TTATCAATCC | AACCAGCAAA | AATAAACAAAG | GAAATGATGT | 360  |
| GGGGACCCAG | TACCGTACTG | GTGTTTATTA | CACAGATGAC | AAGGATTTGG  | AAGTGATTAA | 420  |
| CCAAGTCTTT | GATGAGGTGG | CTAAGAAATA | CGATCAACCT | CTAGCAGTTG  | AAAAGGAAAA | 480  |
| CTTGAAGAAT | TTTGTGGTGG | CTGAGGATTA | CCATCAAGAC | TATCTCAAGA  | AAAATCCAAA | 540  |
| TGGCTACTGC | CATATCAATG | TTAATCAGGC | GGCCTATCCT | GTCATTGATG  | CCAGCAAATA | 600  |
| TCCAAACCA  | AGTGATGAGG | AATTGAAAAA | GACCCTGTCA | CCTGAGGAGT  | ATGCAGTTAC | 660  |
| CCAGGAAAAT | CAAACAGAAC | GAGCTTTCTC | AAACCGTTAC | TGGGATAAAT  | TTGAATCCGG | 720  |
| TATCTATGTG | GATATAGCAA | CTGGGGAACC | TCTCTTTTCA | TCAAAAGACA  | AATTTGAGTC | 780  |
| TGGTTGTGGC | TGGCCTAGTT | TTACCCAACC | CATCAGTCCA | GATGTTGTCA  | CCTACAAGGA | 840  |
| AGATAAGTCC | TACAATATGA | CGCGTATGGA | AGTGCGGAGC | CGAGTAGGAG  | ATTCTCACCT | 900  |
| TGGGCATGTC | TTTACGGATG | GTCCACAGGA | CAAGGGCGGC | TTACGTTACT  | GTATCAATAG | 960  |
| CCTCTCTATC | CGCTTTATTC | CCAAAGACCA | AATGGAAGAA | AAAGGCTACG  | CTTATTTACT | 1020 |
| AGATTATGTT | GAT        |            |            |             |            | 1033 |

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 344 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```

Arg Asn Ala Gly Gln Thr Asp Ala Ser Gln Ile Glu Lys Ala Ala Val
1          5          10          15
Ser Gln Gly Gly Lys Ala Val Lys Lys Thr Glu Ile Ser Lys Asp Ala
20          25          30
Asp Leu His Glu Ile Tyr Leu Ala Gly Gly Cys Phe Trp Gly Val Glu
35          40          45
Glu Tyr Phe Ser Arg Val Pro Gly Val Thr Asp Ala Val Ser Gly Tyr
50          55          60
Ala Asn Gly Arg Gly Glu Thr Thr Lys Tyr Glu Leu Ile Asn Gln Thr
65          70          75          80
Gly His Ala Glu Thr Val His Val Thr Tyr Asp Ala Lys Gln Ile Ser
85          90          95
Leu Lys Glu Ile Leu Leu His Tyr Phe Arg Ile Ile Asn Pro Thr Ser
100         105         110
Lys Asn Lys Gln Gly Asn Asp Val Gly Thr Gln Tyr Arg Thr Gly Val
115         120         125
Tyr Tyr Thr Asp Asp Lys Asp Leu Glu Val Ile Asn Gln Val Phe Asp
130         135         140
Glu Val Ala Lys Lys Tyr Asp Gln Pro Leu Ala Val Glu Lys Glu Asn
145         150         155         160
Leu Lys Asn Phe Val Val Ala Glu Asp Tyr His Gln Asp Tyr Leu Lys
165         170         175
Lys Asn Pro Asn Gly Tyr Cys His Ile Asn Val Asn Gln Ala Ala Tyr
180         185         190
Pro Val Ile Asp Ala Ser Lys Tyr Pro Lys Pro Ser Asp Glu Glu Leu
195         200         205
Lys Lys Thr Leu Ser Pro Glu Glu Tyr Ala Val Thr Gln Glu Asn Gln
210         215         220
Thr Glu Arg Ala Phe Ser Asn Arg Tyr Trp Asp Lys Phe Glu Ser Gly
225         230         235         240
Ile Tyr Val Asp Ile Ala Thr Gly Glu Pro Leu Phe Ser Ser Lys Asp
245         250         255
Lys Phe Glu Ser Gly Cys Gly Trp Pro Ser Phe Thr Gln Pro Ile Ser
260         265         270
Pro Asp Val Val Thr Tyr Lys Glu Asp Lys Ser Tyr Asn Met Thr Arg

```

275                                      280                                      285  
 Met Glu Val Arg Ser Arg Val Gly Asp Ser His Leu Gly His Val Phe  
     290                                      295                                      300  
 Thr Asp Gly Pro Gln Asp Lys Gly Gly Leu Arg Tyr Cys Ile Asn Ser  
     305                                      310                                      315                                      320  
 Leu Ser Ile Arg Phe Ile Pro Lys Asp Gln Met Glu Glu Lys Gly Tyr  
                                     325                                      330                                      335  
 Ala Tyr Leu Leu Asp Tyr Val Asp  
                                     340

## (2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

TGTATAGTTT TTAGCGCTTG TTCTTCTAAT TCTGNTAAAA ATGAAGAAAA TACTTCTAAA 60  
 GAGCATGCGC CTGATAAAAT AGTTTTAGAT CATGCTTTCG GTCAAACCTAT ATTAGATAAA 120  
 AAACCTGAAA GAGTTGCAAC TATTGCTTGG GGAAATCATG ATGTAGCATT AGCTTTAGGA 180  
 ATAGTTCCTG TTGGATTTTC AAAAGCAAAT TACGGTGTA GTGCTGATAA AGGAGTTTTA 240  
 CCATGGACAG AAGAAAAAAT CAAAGAACTA AATGGTAAAG CTAACCTATT TGACGATTTG 300  
 GATGGACTTA ACTTTGAAGC AATATCAAAT TCTAAACCAG ATGTTATCTT AGCAGGTTAT 360  
 TCTGGTATAA CTAAAGAAGA TTATGACACT CTATCA 396

## (2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 132 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Cys Ile Val Phe Ser Ala Cys Ser Ser Asn Ser Xaa Lys Asn Glu Glu  
 1                                      5                                      10                                      15  
 Asn Thr Ser Lys Glu His Ala Pro Asp Lys Ile Val Leu Asp His Ala  
     20                                      25                                      30  
 Phe Gly Gln Thr Ile Leu Asp Lys Lys Pro Glu Arg Val Ala Thr Ile  
     35                                      40                                      45  
 Ala Trp Gly Asn His Asp Val Ala Leu Ala Leu Gly Ile Val Pro Val  
     50                                      55                                      60

Gly Phe Ser Lys Ala Asn Tyr Gly Val Ser Ala Asp Lys Gly Val Leu  
 65 70 75 80  
 Pro Trp Thr Glu Glu Lys Ile Lys Glu Leu Asn Gly Lys Ala Asn Leu  
 85 90 95  
 Phe Asp Asp Leu Asp Gly Leu Asn Phe Glu Ala Ile Ser Asn Ser Lys  
 100 105 110  
 Pro Asp Val Ile Leu Ala Gly Tyr Ser Gly Ile Thr Lys Glu Asp Tyr  
 115 120 125  
 Asp Thr Leu Ser  
 130

## (2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 844 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTGTGTCGAG CATATTCTGA AGCAAACCTA TCAAAATATA GAAATTATTT TAGTTGATGA | 60  |
| CGGTTCTACG GATAATTCTG GGGAAATTTG TGATGCTTTT ATGATGCAAG ATAATCGTGT | 120 |
| GCGAGTATTG CATCAAGAAA ATAAGGGGGG GGCAGCACAA GCTAAAAATA TGGGGATTAG | 180 |
| TGTAGCTAAG GGAGAGTACA TCACGATTGT TGATTCAGAT GATATCGTAA AAGAAAATAT | 240 |
| GATTGAAACT CTTTATCAGC AAGTCCAAGA AAAGGATGCA GATGTTGTTA TAGGGAATTA | 300 |
| CTATAATTAT GACGAAAGTG ACGGGAATTT TTATTTTAT GTAACAGGGC AAGATTTTTG  | 360 |
| CGTCGAAGAA TTAGCTATAC AAGAAATTAT GAACCGTCAA GCAGGAGATT GGAAATTCAA | 420 |
| TAGCTCGGCC TTTATATTGC CGACATTTAA GTTGATTAAA AAAGAATTAT TCAATGAAGT | 480 |
| TCACTTTTCA AATGGTCGCC GCTTTGATGA TGAAGCAACT ATGCATCGCT TTTATCTTTT | 540 |
| AGCCTCTAAA ATCGTCTTTA TAAACGATAA TCTCTATCTG TATAGAAGAC GTTCAGGAAG | 600 |
| CATCATGAGA ACGGAATTTG ATCTTTCCTG GGCAAGAGAT ATTGTTGAAG TGTTTCTAA  | 660 |
| GAAAATATCG GATTGTGTCT TGGCTGGTTT GGATGTCTCC GTTCTGCGTA TTCGATTGT  | 720 |
| CAATCTTTTA AAAGATTATA AGCAAACCTT AGAATACCAT CAATTAACAG ATACTGAGGA | 780 |
| ATATAAAGAT ATTTGTTTCA GATTAAAGTT GTTTTTTGAT GCAGAACAAA GAAATGGTAA | 840 |
| AAGT                                                              | 844 |

## (2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 281 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Val | Glu | His | Ile | Leu | Lys | Gln | Thr | Tyr | Gln | Asn | Ile | Glu | Ile | Ile | 1   | 5   | 10  | 15  |
| Leu | Val | Asp | Asp | Gly | Ser | Thr | Asp | Asn | Ser | Gly | Glu | Ile | Cys | Asp | Ala | 20  | 25  | 30  |     |
| Phe | Met | Met | Gln | Asp | Asn | Arg | Val | Arg | Val | Leu | His | Gln | Glu | Asn | Lys | 35  | 40  | 45  |     |
| Gly | Gly | Ala | Ala | Gln | Ala | Lys | Asn | Met | Gly | Ile | Ser | Val | Ala | Lys | Gly | 50  | 55  | 60  |     |
| Glu | Tyr | Ile | Thr | Ile | Val | Asp | Ser | Asp | Asp | Ile | Val | Lys | Glu | Asn | Met | 65  | 70  | 75  | 80  |
| Ile | Glu | Thr | Leu | Tyr | Gln | Gln | Val | Gln | Glu | Lys | Asp | Ala | Asp | Val | Val | 85  | 90  | 95  |     |
| Ile | Gly | Asn | Tyr | Tyr | Asn | Tyr | Asp | Glu | Ser | Asp | Gly | Asn | Phe | Tyr | Phe | 100 | 105 | 110 |     |
| Tyr | Val | Thr | Gly | Gln | Asp | Phe | Cys | Val | Glu | Glu | Leu | Ala | Ile | Gln | Glu | 115 | 120 | 125 |     |
| Ile | Met | Asn | Arg | Gln | Ala | Gly | Asp | Trp | Lys | Phe | Asn | Ser | Ser | Ala | Phe | 130 | 135 | 140 |     |
| Ile | Leu | Pro | Thr | Phe | Lys | Leu | Ile | Lys | Lys | Glu | Leu | Phe | Asn | Glu | Val | 145 | 150 | 155 | 160 |
| His | Phe | Ser | Asn | Gly | Arg | Arg | Phe | Asp | Asp | Glu | Ala | Thr | Met | His | Arg | 165 | 170 | 175 |     |
| Phe | Tyr | Leu | Leu | Ala | Ser | Lys | Ile | Val | Phe | Ile | Asn | Asp | Asn | Leu | Tyr | 180 | 185 | 190 |     |
| Leu | Tyr | Arg | Arg | Arg | Ser | Gly | Ser | Ile | Met | Arg | Thr | Glu | Phe | Asp | Leu | 195 | 200 | 205 |     |
| Ser | Trp | Ala | Arg | Asp | Ile | Val | Glu | Val | Phe | Ser | Lys | Lys | Ile | Ser | Asp | 210 | 215 | 220 |     |
| Cys | Val | Leu | Ala | Gly | Leu | Asp | Val | Ser | Val | Leu | Arg | Ile | Arg | Phe | Val | 225 | 230 | 235 | 240 |
| Asn | Leu | Leu | Lys | Asp | Tyr | Lys | Gln | Thr | Leu | Glu | Tyr | His | Gln | Leu | Thr | 245 | 250 | 255 |     |
| Asp | Thr | Glu | Glu | Tyr | Lys | Asp | Ile | Cys | Phe | Arg | Leu | Lys | Leu | Phe | Phe | 260 | 265 | 270 |     |
| Asp | Ala | Glu | Gln | Arg | Asn | Gly | Lys | Ser | 275 | 280 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

```

GTGTTTGGAT AGCATTTCAGA ATCAGACGTA TCAAAATTTT GAGTGTTTAT TAATCAATGA      60
TGGCTCTCCA GATCATTCAT CCAAATATG TGAAGAATTT GTAGAGAAAG ATTCTCGTTT      120
CAAATATTTT GAGAAAGCAA ACGGCGGTCT TTCATCAGCT CGTAACCTAG GTATTGAATG      180
TTCGGGGGGG GCGTACATTA CTTTGTAGA CTCTGATGAT TGGTTGGAAC ATGATGCTTT      240
AGACCGATTA TATGGTGCTT TGAAAAAGGA AAACGCAGAT ATTAGTATCG GGC GTTATAA      300
TTCTTATGAT GAAACACGCT ATGTGTATAT GACTTATGTT ACGGATCCAG ATGATTCTCT      360
AGAAGTGATA GAAGGTAAAG CAATTATGGA TAGGGAAGGT GTCGAAGAAG TCAGAAATGG      420
GAACTGGACT GTAGCTGTCT TGAAGTTATT CAAGAGAGAG TTA CTACAAG ATTTACCATT      480
TCCTATAGGA AAAATTGCAG AGGATACTTA CTGGACATGG AAGGTACTTC TAAGAGCTTC      540
GAGGATAGTC TATTTGAATC GTTGTGTTTA CTGGTACCGT GTTGGTTTAT CTGATACTTT      600
ATCGAATACA TGGAGTGAAA AGCGTATGTA TGATGAAATT GGGGCTAGGG AAGAAAAGAT      660
AGCTATTTTA GCAAGTTCAG ACTATGACTT GACCAATCAT ATTTTGATTT ATAAAAATAG      720
ATTACAAAGA GTGATAGCAA AATTAGAAGA ACAAATATG CAGTTCACAG AGATTTACAG      780
AAGAATGATG GAAAAATTGT CTTTACTTCC G      811

```

## (2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 270 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

```

Cys Leu Asp Ser Ile Gln Asn Gln Thr Tyr Gln Asn Phe Glu Cys Leu
1           5           10           15
Leu Ile Asn Asp Gly Ser Pro Asp His Ser Ser Lys Ile Cys Glu Glu
20          25          30
Phe Val Glu Lys Asp Ser Arg Phe Lys Tyr Phe Glu Lys Ala Asn Gly
35          40          45
Gly Leu Ser Ser Ala Arg Asn Leu Gly Ile Glu Cys Ser Gly Gly Ala
50          55          60
Tyr Ile Thr Phe Val Asp Ser Asp Asp Trp Leu Glu His Asp Ala Leu
65          70          75          80

```

Asp Arg Leu Tyr Gly Ala Leu Lys Lys Glu Asn Ala Asp Ile Ser Ile  
                     85                    90                    95  
 Gly Arg Tyr Asn Ser Tyr Asp Glu Thr Arg Tyr Val Tyr Met Thr Tyr  
                     100                    105                    110  
 Val Thr Asp Pro Asp Asp Ser Leu Glu Val Ile Glu Gly Lys Ala Ile  
                     115                    120                    125  
 Met Asp Arg Glu Gly Val Glu Glu Val Arg Asn Gly Asn Trp Thr Val  
                     130                    135                    140  
 Ala Val Leu Lys Leu Phe Lys Arg Glu Leu Leu Gln Asp Leu Pro Phe  
                     145                    150                    155                    160  
 Pro Ile Gly Lys Ile Ala Glu Asp Thr Tyr Trp Thr Trp Lys Val Leu  
                     165                    170                    175  
 Leu Arg Ala Ser Arg Ile Val Tyr Leu Asn Arg Cys Val Tyr Trp Tyr  
                     180                    185                    190  
 Arg Val Gly Leu Ser Asp Thr Leu Ser Asn Thr Trp Ser Glu Lys Arg  
                     195                    200                    205  
 Met Tyr Asp Glu Ile Gly Ala Arg Glu Glu Lys Ile Ala Ile Leu Ala  
                     210                    215                    220  
 Ser Ser Asp Tyr Asp Leu Thr Asn His Ile Leu Ile Tyr Lys Asn Arg  
                     225                    230                    235                    240  
 Leu Gln Arg Val Ile Ala Lys Leu Glu Glu Gln Asn Met Gln Phe Thr  
                     245                    250                    255  
 Glu Ile Tyr Arg Arg Met Met Glu Lys Leu Ser Leu Leu Pro  
                     260                    265                    270

## (2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2023 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTGCCTAGAT AGTATTATTA CTCAAACATA TAAAAATATT GAGATTGTTG TCGTTAATGA | 60  |
| TGGTTCTACG GATGCTTCAG GTGAAATTTG TAAAGAATTT TCAGAAATGG ATCACCGAAT | 120 |
| TCTCTATATA GAACAAGAAA ATGCTGGTCT TTCTGCCGCA CGAAACACCG GTCTGAATAA | 180 |
| TATGTCCGGA AATTATGTGA CCTTTGTGGA CTCGGATGAT TGGATTGAGC AAGATTATGT | 240 |
| AGAAACTCTA TATAAAAAAA TAGTAGAGTA TCAGGCTGAT ATTGCAGTTG GTAATTATTA | 300 |
| TTCTTTCAAC GAAAGTGAAG GAATGTTCTA CTTTCATATA TTGGGAGACT CCTATTATGA | 360 |
| GAAAGTATAT GATAATGTTT CTATCTTTGA GAACTTGTAT GAAACTCAAG AAATGAAGAG | 420 |
| TTTTGCTTTG ATATCTGCTT GGGGTAACT CTATAAGGCA AGATTGTTTG AGCAGTTGCG  | 480 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| CTTTGACATA GGTAAATTAG GAGAAGATGG TTACCTCAAT CAAAAGGTAT ATTTATTATC | 540  |
| AGAAAAGGTA ATTTATTTAA ATAAAAGTCT TTATGCTTAT CGGATTAGAA AAGGTAGTTT | 600  |
| ATCAAGAGTT TGGACAGAAA AGTGGATGCA CGCTTTAGTT GATGCTATGT CTGAACGTAT | 660  |
| TACGCTACTA GCTAATATGG GTTATCCTCT AGAGAAACAC TTGGCAGTTT ATCGTCAGAT | 720  |
| GTTGGAAGTC AGTCTCGCCA ACGGTCAAGC TAGTGGTTTA TCTGACACAG CAACGTATAA | 780  |
| AGAGTTTGAA ATGAAACAAA GGCTTTTAAA TCAGCTATCG AGACAAGAGG AAAGTGAAAA | 840  |
| GAAAGCCATT GTCCTCGCAG CAAACTATGG CTATGTAGAC CAAGTTTTAA CGACAATCAA | 900  |
| GTCTATTTGT TATCATAATC GTTCGATTCG TTTTATCTG ATTCATAGCG ATTTTCCAAA  | 960  |
| TGAATGGATT AAGCAATTAA ATAAGCGCTT AGAGAAGTTT GACTCAGAAA TTATTAATTG | 1020 |
| TCGGGTAACT TCTGAGCAAA TTTCATGTTA TAAATCGGAT ATTAGTTACA CAGTCTTTTT | 1080 |
| ACGCTATTTT ATAGCTGATT TCGTGCAAGA AGACAAGGCC CTCTACTTGG ACTGTGATCT | 1140 |
| AGTTGTAACG AAAAATCTGG ATGACTTGTT TGCTACAGAC TTACAAGATT ATCCTTTGGC | 1200 |
| TGCTGTTAGA GATTTTGGGG GCAGAGCTTA TTTTGGTCAA GAAATCTTTA ATGCCGGTGT | 1260 |
| TCTCTTGGTA AACAATGCCT TTTGGAAAAA AGAGAATATG ACCCAAAAAT TAATTGATGT | 1320 |
| AACCAATGAA TGGCATGATA AGGTGGATCA GGCAGATCAG AGCATCTTGA ATATGCTTTT | 1380 |
| TGAACATAAA TGGTTGGAAT TGGACTTTGA TTATAATCAT ATTGTCATTC ATAAACAGTT | 1440 |
| TGCTGATTAT CAATTGCCTG AGGGTCAGGA TTATCCTGCT ATTATTCACT ATCTTTCTCA | 1500 |
| TCGGAAACCG TGGAAGATT TGGCGGCCCA AACCTATCGT GAAGTTTGGT GGTACTATCA  | 1560 |
| TGGGCTTGAA TGGACAGAAT TGGGACAAAA CCATCATTTA CATCCATTAC AAAGATCTCA | 1620 |
| CATCTATCCA ATAAAGGAAC CTTTCACTTG TCTAATCTAT ACTGCCTCAG ACCATATTGA | 1680 |
| ACAAATTGAG ACATTGGTTC AATCCTTGCC TGATATTCAG TTTAAGATAG CAGCTAGAGT | 1740 |
| AATAGTTAGT GATCGATTGG CTCAGATGAC AATTATCCA AACGTGACTA TATTTAACGG  | 1800 |
| AATTCACTAT TTGGTAGATG TCGATAATGA ATTGGTAGAA ACCAGTCAAG TACTTTTAGA | 1860 |
| TATTAATCAT GGCGAAAAGA CAGAAGAAAT TCTCGATCAA TTTGCTAATC TTGGCAAGCC | 1920 |
| TATCTTATCC TTTGAAAATA CTAAACCTA TGAAGTAGGT CAGGAGGCAT ATGCTGTTGA  | 1980 |
| CCAAGTTCAA GCAATGATTG AAAAATTGAG AGAAATAAGC AAA                   | 2023 |

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Cys Leu Asp Ser Ile Ile Thr Gln Thr Tyr Lys Asn Ile Glu Ile Val  
 1 5 10 15  
 Val Val Asn Asp Gly Ser Thr Asp Ala Ser Gly Glu Ile Cys Lys Glu  
 20 25 30  
 Phe Ser Glu Met Asp His Arg Ile Leu Tyr Ile Glu Gln Glu Asn Ala  
 35 40 45  
 Gly Leu Ser Ala Ala Arg Asn Thr Gly Leu Asn Asn Met Ser Gly Asn  
 50 55 60  
 Tyr Val Thr Phe Val Asp Ser Asp Asp Trp Ile Glu Gln Asp Tyr Val  
 65 70 75 80  
 Glu Thr Leu Tyr Lys Lys Ile Val Glu Tyr Gln Ala Asp Ile Ala Val  
 85 90 95  
 Gly Asn Tyr Tyr Ser Phe Asn Glu Ser Glu Gly Met Phe Tyr Phe His  
 100 105 110  
 Ile Leu Gly Asp Ser Tyr Tyr Glu Lys Val Tyr Asp Asn Val Ser Ile  
 115 120 125  
 Phe Glu Asn Leu Tyr Glu Thr Gln Glu Met Lys Ser Phe Ala Leu Ile  
 130 135 140  
 Ser Ala Trp Gly Lys Leu Tyr Lys Ala Arg Leu Phe Glu Gln Leu Arg  
 145 150 155 160  
 Phe Asp Ile Gly Lys Leu Gly Glu Asp Gly Tyr Leu Asn Gln Lys Val  
 165 170 175  
 Tyr Leu Leu Ser Glu Lys Val Ile Tyr Leu Asn Lys Ser Leu Tyr Ala  
 180 185 190  
 Tyr Arg Ile Arg Lys Gly Ser Leu Ser Arg Val Trp Thr Glu Lys Trp  
 195 200 205  
 Met His Ala Leu Val Asp Ala Met Ser Glu Arg Ile Thr Leu Leu Ala  
 210 215 220  
 Asn Met Gly Tyr Pro Leu Glu Lys His Leu Ala Val Tyr Arg Gln Met  
 225 230 235 240  
 Leu Glu Val Ser Leu Ala Asn Gly Gln Ala Ser Gly Leu Ser Asp Thr  
 245 250 255  
 Ala Thr Tyr Lys Glu Phe Glu Met Lys Gln Arg Leu Leu Asn Gln Leu  
 260 265 270  
 Ser Arg Gln Glu Glu Ser Glu Lys Lys Ala Ile Val Leu Ala Ala Asn  
 275 280 285  
 Tyr Gly Tyr Val Asp Gln Val Leu Thr Thr Ile Lys Ser Ile Cys Tyr  
 290 295 300  
 His Asn Arg Ser Ile Arg Phe Tyr Leu Ile His Ser Asp Phe Pro Asn  
 305 310 315 320  
 Glu Trp Ile Lys Gln Leu Asn Lys Arg Leu Glu Lys Phe Asp Ser Glu  
 325 330 335

Ile Ile Asn Cys Arg Val Thr Ser Glu Gln, Ile Ser Cys Tyr Lys Ser  
 340 345 350  
 Asp Ile Ser Tyr Thr Val Phe Leu Arg Tyr Phe Ile Ala Asp Phe Val  
 355 360 365  
 Gln Glu Asp Lys Ala Leu Tyr Leu Asp Cys Asp Leu Val Val Thr Lys  
 370 375 380  
 Asn Leu Asp Asp Leu Phe Ala Thr Asp Leu Gln Asp Tyr Pro Leu Ala  
 385 390 395 400  
 Ala Val Arg Asp Phe Gly Gly Arg Ala Tyr Phe Gly Gln Glu Ile Phe  
 405 410 415  
 Asn Ala Gly Val Leu Leu Val Asn Asn Ala Phe Trp Lys Lys Glu Asn  
 420 425 430  
 Met Thr Gln Lys Leu Ile Asp Val Thr Asn Glu Trp His Asp Lys Val  
 435 440 445  
 Asp Gln Ala Asp Gln Ser Ile Leu Asn Met Leu Phe Glu His Lys Trp  
 450 455 460  
 Leu Glu Leu Asp Phe Asp Tyr Asn His Ile Val Ile His Lys Gln Phe  
 465 470 475 480  
 Ala Asp Tyr Gln Leu Pro Glu Gly Gln Asp Tyr Pro Ala Ile Ile His  
 485 490 495  
 Tyr Leu Ser His Arg Lys Pro Trp Lys Asp Leu Ala Ala Gln Thr Tyr  
 500 505 510  
 Arg Glu Val Trp Trp Tyr Tyr His Gly Leu Glu Trp Thr Glu Leu Gly  
 515 520 525  
 Gln Asn His His Leu His Pro Leu Gln Arg Ser His Ile Tyr Pro Ile  
 530 535 540  
 Lys Glu Pro Phe Thr Cys Leu Ile Tyr Thr Ala Ser Asp His Ile Glu  
 545 550 555 560  
 Gln Ile Glu Thr Leu Val Gln Ser Leu Pro Asp Ile Gln Phe Lys Ile  
 565 570 575  
 Ala Ala Arg Val Ile Val Ser Asp Arg Leu Ala Gln Met Thr Ile Tyr  
 580 585 590  
 Pro Asn Val Thr Ile Phe Asn Gly Ile His Tyr Leu Val Asp Val Asp  
 595 600 605  
 Asn Glu Leu Val Glu Thr Ser Gln Val Leu Leu Asp Ile Asn His Gly  
 610 615 620  
 Glu Lys Thr Glu Glu Ile Leu Asp Gln Phe Ala Asn Leu Gly Lys Pro  
 625 630 635 640  
 Ile Leu Ser Phe Glu Asn Thr Lys Thr Tyr Glu Val Gly Gln Glu Ala  
 645 650 655  
 Tyr Ala Val Asp Gln Val Gln Ala Met Ile Glu Lys Leu Arg Glu Ile  
 660 665 670

Ser Lys

## (2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 910 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| CATTCAGAAG CAGACCTATC AAAATCTGGA AATTATTCTT GTTGATGATG GTGCAACAGA   | 60  |
| TGAAAGTGGT CGCTTGTGTG ATTCAATCGC TGAACAAGAT GACAGGGTGT CAGTGCTTCA   | 120 |
| TAAAAAGAAC GAAGGATTGT CGCAAGCACG AAATGATGGG ATGAAGCAGG CTCACGGGGA   | 180 |
| TTATCTGATT TTTATTGACT CAGATGATTA TATCCATCCA GAAATGATTC AGAGCTTATA   | 240 |
| TGAGCAATTA GTTCAAGAAG ATGCGGATGT TTCGAGCTGT GGTGTCATGA ATGTCTATGC   | 300 |
| TAATGATGAA AGCCACAGT CAGCCAATCA GGATGACTAT TTTGTCTGTG ATTCTCAAAC    | 360 |
| ATTTCTAAAG GAATACCTCA TAGGTGAAAA AATACCTGGG ACGATTGCA ATAAGCTAAT    | 420 |
| CAAGAGACAG ATTGCAACTG CCCTATCCTT TCCTAAGGGG TTGATTTACG AAGATGCCTA   | 480 |
| TTACCATTTT GATTTAATCA AGTTGGCCAA GAAGTATGTG GTTAATACTA AACCCATTATTA | 540 |
| TTACTATTTT CATAGAGGGG ATAGTATTAC GACCAAACCC TATGCAGAGA AGGATTTAGC   | 600 |
| CTATATTGAT ATCTACCAA AGTTTTATAA TGAAGTTGTG AAAAATATC CTGACTTGAA     | 660 |
| AGAGGTCGCT TTTTTCAGAT TGGCCTATGC CCACTTCTTT ATTCTGGATA AGATGTTGCT   | 720 |
| AGATGATCAG TATAAACAGT TTGAAGCCTA TTCTCAGATT CATCGTTTTT TAAAAGGCCA   | 780 |
| TGCCTTTGCT ATTTCTAGGA ATCCAATTTT CCGTAAGGGG AGAAGAATTA GTGCTTTGGC   | 840 |
| CCTATTCATA AATATTTCTT TATATCGATT CTTATTACTG AAAAATATTG AAAAATCTAA   | 900 |
| AAAATTACAT                                                          | 910 |

## (2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 303 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Gln | Lys | Gln | Thr | Tyr | Gln | Asn | Leu | Glu | Ile | Ile | Leu | Val | Asp | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ala | Thr | Asp | Glu | Ser | Gly | Arg | Leu | Cys | Asp | Ser | Ile | Ala | Glu | Gln |

| 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Asp | Arg | Val | Ser | Val | Leu | His | Lys | Lys | Asn | Glu | Gly | Leu | Ser | Gln |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Arg | Asn | Asp | Gly | Met | Lys | Gln | Ala | His | Gly | Asp | Tyr | Leu | Ile | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Asp | Ser | Asp | Asp | Tyr | Ile | His | Pro | Glu | Met | Ile | Gln | Ser | Leu | Tyr |
|     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Glu | Gln | Leu | Val | Gln | Glu | Asp | Ala | Asp | Val | Ser | Ser | Cys | Gly | Val | Met |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Val | Tyr | Ala | Asn | Asp | Glu | Ser | Pro | Gln | Ser | Ala | Asn | Gln | Asp | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Phe | Val | Cys | Asp | Ser | Gln | Thr | Phe | Leu | Lys | Glu | Tyr | Leu | Ile | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Lys | Ile | Pro | Gly | Thr | Ile | Cys | Asn | Lys | Leu | Ile | Lys | Arg | Gln | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Thr | Ala | Leu | Ser | Phe | Pro | Lys | Gly | Leu | Ile | Tyr | Glu | Asp | Ala | Tyr |
|     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Tyr | His | Phe | Asp | Leu | Ile | Lys | Leu | Ala | Lys | Lys | Tyr | Val | Val | Asn | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Pro | Tyr | Tyr | Tyr | Tyr | Phe | His | Arg | Gly | Asp | Ser | Ile | Thr | Thr | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Tyr | Ala | Glu | Lys | Asp | Leu | Ala | Tyr | Ile | Asp | Ile | Tyr | Gln | Lys | Phe |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Asn | Glu | Val | Val | Lys | Asn | Tyr | Pro | Asp | Leu | Lys | Glu | Val | Ala | Phe |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Arg | Leu | Ala | Tyr | Ala | His | Phe | Phe | Ile | Leu | Asp | Lys | Met | Leu | Leu |
|     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Asp | Asp | Gln | Tyr | Lys | Gln | Phe | Glu | Ala | Tyr | Ser | Gln | Ile | His | Arg | Phe |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Lys | Gly | His | Ala | Phe | Ala | Ile | Ser | Arg | Asn | Pro | Ile | Phe | Arg | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Arg | Arg | Ile | Ser | Ala | Leu | Ala | Leu | Phe | Ile | Asn | Ile | Ser | Leu | Tyr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Phe | Leu | Leu | Leu | Lys | Asn | Ile | Glu | Lys | Ser | Lys | Lys | Leu | His |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| TAAGGCTGAT AATCGTGTTC AAATGAGAAC GACGATTAAT AATGAATCGC CATTGTTGCT | 60   |
| TTCTCCGTTG TATGGCAATG ATAATGGTAA CGGATTATGG TGGGGGAACA CATTGAAGGG | 120  |
| AGCATGGGAA GCTATTCCTG AAGATGTAAA GCCATATGCA GCGATTGAAC TTCATCCTGC | 180  |
| AAAAGTCTGT AAACCAACAA GTTGTATTCC ACGAGATACG AAAGAATTGA GAGAATGGTA | 240  |
| TGTCAAGATG TTGGAGGAAG CTCAAAGTCT AAACATTCCA GTTTTCTTGG TTATTATGTC | 300  |
| GGCTGGAGAG CGTAATACAG TTCCTCCAGA GTGGTTAGAT GAACAATTCC AAAAGTATAG | 360  |
| TGTGTTAAAA GGTGTTTTAA ATATTGAGAA TTATTGGATT TACAATAACC AGTTAGCTCC | 420  |
| GCATAGTGCT AAATATTTGG AAGTTTGTGC CAAATATGGA GCGCATTTTA TCTGGCATGA | 480  |
| TCATGAAAAA TGGTTCTGGG AAACATTAT GAATGATCCG ACATTCTTTG AAGCGAGTCA  | 540  |
| AAAATATCAT AAAAATTTGG TGTGGCAAC TAAAAATACG CCAATAAGAG ATGATGCGGG  | 600  |
| TACAGATTCT ATCGTTAGTG GATTTTGGTT GAGTGGCTTA TGTGATAACT GGGGCTCATC | 660  |
| AACAGATACA TGGAAATGGT GGGAAAAACA TTATACAAAC ACATTTGAAA CTGGAAGAGC | 720  |
| TAGGGATATG AGATCCTATG CATCGGAACC AGAATCAATG ATTGCTATGG AAATGATGAA | 780  |
| TGTATATACT GGGGGAGGCA CAGTTTATAA TTTCGAATGT GCCGCGTATA CATTTATGAC | 840  |
| AAATGATGTA CCAACTCCAG CATTTACTAA AGGTATTATT CCTTTCTTTA GACATGCTAT | 900  |
| ACAAAATCCA GCTCCAAGTA AGGAAGAAGT TGTAATAGA ACAAAGCTG TATTTTGGAA   | 960  |
| TGGAGAAGGT AGGATTAGTT CATTAAACGG ATTTTATCAA GGACTTTATT CGAATGATGA | 1020 |
| AACAATGCCT TTATATAATA ATGGGAGATA TCATATTCTT CCTGTAATAC ATGAGAAAAT | 1080 |
| TGATAAGGAA AAGATTTTAT CTATATTTCC TAATGCAAAA ATTTTGACTA AAAATAGTGA | 1140 |
| GGAATTGTCT AGTAAAGTCA ACTATTTAAA CTCGCTTTAT CCAAACTTT ATGAAGGAGA  | 1200 |
| TGGGTATGCT CAGCGTGTAG GTAATTCCTG GTATATTTAT AATAGTAATG CTAATATCAA | 1260 |
| TAAAAATCAG CAAGTAATGT TGCCTATGTA TACTAATAAT ACAAAGTCGT TATCGTTAGA | 1320 |
| TTTGACGCCA CATACTTACG CTGTTGTTAA AGAAAATCCA AATAATTTAC ATATTTTATT | 1380 |
| GAATAATTAC AGGACAGATA AGACAGCTAT GTGGGCATTA TCAGGAAATT TTGATGCATC | 1440 |
| AAAAAGTTGG AAGAAAGAAG AATTAGAGTT AGCGAACTGG ATAAGCAAAA ATTATTCCAT | 1500 |
| CAATCCTGTA GATAATGACT TTAGGACAAC AACACTTACA TTAAAAGGGC ATACTGGTCA | 1560 |
| TAAACCTCAG ATAAATATAA GTGGCGATAA AAATCATTAT ACTTATACAG AAAATTGGGA | 1620 |
| TGAGAATACC CATGTTTATA CCATTACGGT TAATCATAAT GGAATGGTAG AGATGTCTAT | 1680 |
| AAATACTGAG GGGACAGGTC CAGTCTCTTT CCCAACACCA GATAAATTTA ATGATGGTAA | 1740 |
| TTTGAATATA GCATATGCAA AACCAACAAC ACAAAGTTCT GTAGATTACA ATGGAGACCC | 1800 |
| TAATAGAGCT GTGGATGGTA ACAGAAATGG TAATTTTAAC TCTGGTTCGG TAACACACAC | 1860 |
| TAGGGCAGAT AATCCCTCTT GGTGGGAAGT CGATTTGAAA AAAATGGATA AAGTTGGGCT | 1920 |

TGTTAAAATT TATAATCGCA CAGATGCTGA GACTCAACGT CTATCTAATT TT

1972

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 657 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Asp | Asn | Arg | Val | Gln | Met | Arg | Thr | Thr | Ile | Asn | Asn | Glu | Ser | 1   | 5   | 10  | 15  |
| Pro | Leu | Leu | Leu | Ser | Pro | Leu | Tyr | Gly | Asn | Asp | Asn | Gly | Asn | Gly | Leu | 20  | 25  | 30  |     |
| Trp | Trp | Gly | Asn | Thr | Leu | Lys | Gly | Ala | Trp | Glu | Ala | Ile | Pro | Glu | Asp | 35  | 40  | 45  |     |
| Val | Lys | Pro | Tyr | Ala | Ala | Ile | Glu | Leu | His | Pro | Ala | Lys | Val | Cys | Lys | 50  | 55  | 60  |     |
| Pro | Thr | Ser | Cys | Ile | Pro | Arg | Asp | Thr | Lys | Glu | Leu | Arg | Glu | Trp | Tyr | 65  | 70  | 75  | 80  |
| Val | Lys | Met | Leu | Glu | Glu | Ala | Gln | Ser | Leu | Asn | Ile | Pro | Val | Phe | Leu | 85  | 90  | 95  |     |
| Val | Ile | Met | Ser | Ala | Gly | Glu | Arg | Asn | Thr | Val | Pro | Pro | Glu | Trp | Leu | 100 | 105 | 110 |     |
| Asp | Glu | Gln | Phe | Gln | Lys | Tyr | Ser | Val | Leu | Lys | Gly | Val | Leu | Asn | Ile | 115 | 120 | 125 |     |
| Glu | Asn | Tyr | Trp | Ile | Tyr | Asn | Asn | Gln | Leu | Ala | Pro | His | Ser | Ala | Lys | 130 | 135 | 140 |     |
| Tyr | Leu | Glu | Val | Cys | Ala | Lys | Tyr | Gly | Ala | His | Phe | Ile | Trp | His | Asp | 145 | 150 | 155 | 160 |
| His | Glu | Lys | Trp | Phe | Trp | Glu | Thr | Ile | Met | Asn | Asp | Pro | Thr | Phe | Phe | 165 | 170 | 175 |     |
| Glu | Ala | Ser | Gln | Lys | Tyr | His | Lys | Asn | Leu | Val | Leu | Ala | Thr | Lys | Asn | 180 | 185 | 190 |     |
| Thr | Pro | Ile | Arg | Asp | Asp | Ala | Gly | Thr | Asp | Ser | Ile | Val | Ser | Gly | Phe | 195 | 200 | 205 |     |
| Trp | Leu | Ser | Gly | Leu | Cys | Asp | Asn | Trp | Gly | Ser | Ser | Thr | Asp | Thr | Trp | 210 | 215 | 220 |     |
| Lys | Trp | Trp | Glu | Lys | His | Tyr | Thr | Asn | Thr | Phe | Glu | Thr | Gly | Arg | Ala | 225 | 230 | 235 | 240 |
| Arg | Asp | Met | Arg | Ser | Tyr | Ala | Ser | Glu | Pro | Glu | Ser | Met | Ile | Ala | Met | 245 | 250 | 255 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Met | Met | Asn | Val | Tyr | Thr | Gly | Gly | Gly | Thr | Val | Tyr | Asn | Phe | Glu | 260 | 265 | 270 |
| Cys | Ala | Ala | Tyr | Thr | Phe | Met | Thr | Asn | Asp | Val | Pro | Thr | Pro | Ala | Phe | 275 | 280 | 285 |
| Thr | Lys | Gly | Ile | Ile | Pro | Phe | Phe | Arg | His | Ala | Ile | Gln | Asn | Pro | Ala | 290 | 295 | 300 |
| Pro | Ser | Lys | Glu | Glu | Val | Val | Asn | Arg | Thr | Lys | Ala | Val | Phe | Trp | Asn | 305 | 310 | 315 |
| Gly | Glu | Gly | Arg | Ile | Ser | Ser | Leu | Asn | Gly | Phe | Tyr | Gln | Gly | Leu | Tyr | 325 | 330 | 335 |
| Ser | Asn | Asp | Glu | Thr | Met | Pro | Leu | Tyr | Asn | Asn | Gly | Arg | Tyr | His | Ile | 340 | 345 | 350 |
| Leu | Pro | Val | Ile | His | Glu | Lys | Ile | Asp | Lys | Glu | Lys | Ile | Ser | Ser | Ile | 355 | 360 | 365 |
| Phe | Pro | Asn | Ala | Lys | Ile | Leu | Thr | Lys | Asn | Ser | Glu | Glu | Leu | Ser | Ser | 370 | 375 | 380 |
| Lys | Val | Asn | Tyr | Leu | Asn | Ser | Leu | Tyr | Pro | Lys | Leu | Tyr | Glu | Gly | Asp | 385 | 390 | 395 |
| Gly | Tyr | Ala | Gln | Arg | Val | Gly | Asn | Ser | Trp | Tyr | Ile | Tyr | Asn | Ser | Asn | 405 | 410 | 415 |
| Ala | Asn | Ile | Asn | Lys | Asn | Gln | Gln | Val | Met | Leu | Pro | Met | Tyr | Thr | Asn | 420 | 425 | 430 |
| Asn | Thr | Lys | Ser | Leu | Ser | Leu | Asp | Leu | Thr | Pro | His | Thr | Tyr | Ala | Val | 435 | 440 | 445 |
| Val | Lys | Glu | Asn | Pro | Asn | Asn | Leu | His | Ile | Leu | Leu | Asn | Asn | Tyr | Arg | 450 | 455 | 460 |
| Thr | Asp | Lys | Thr | Ala | Met | Trp | Ala | Leu | Ser | Gly | Asn | Phe | Asp | Ala | Ser | 465 | 470 | 475 |
| Lys | Ser | Trp | Lys | Lys | Glu | Glu | Leu | Glu | Leu | Ala | Asn | Trp | Ile | Ser | Lys | 485 | 490 | 495 |
| Asn | Tyr | Ser | Ile | Asn | Pro | Val | Asp | Asn | Asp | Phe | Arg | Thr | Thr | Thr | Leu | 500 | 505 | 510 |
| Thr | Leu | Lys | Gly | His | Thr | Gly | His | Lys | Pro | Gln | Ile | Asn | Ile | Ser | Gly | 515 | 520 | 525 |
| Asp | Lys | Asn | His | Tyr | Thr | Tyr | Thr | Glu | Asn | Trp | Asp | Glu | Asn | Thr | His | 530 | 535 | 540 |
| Val | Tyr | Thr | Ile | Thr | Val | Asn | His | Asn | Gly | Met | Val | Glu | Met | Ser | Ile | 545 | 550 | 555 |
| Asn | Thr | Glu | Gly | Thr | Gly | Pro | Val | Ser | Phe | Pro | Thr | Pro | Asp | Lys | Phe | 565 | 570 | 575 |
| Asn | Asp | Gly | Asn | Leu | Asn | Ile | Ala | Tyr | Ala | Lys | Pro | Thr | Thr | Gln | Ser | 580 | 585 | 590 |
| Ser | Val | Asp | Tyr | Asn | Gly | Asp | Pro | Asn | Arg | Ala | Val | Asp | Gly | Asn | Arg |     |     |     |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 595                                                             | 600 | 605 |
| Asn Gly Asn Phe Asn Ser Gly Ser Val Thr His Thr Arg Ala Asp Asn |     |     |
| 610                                                             | 615 | 620 |
| Pro Ser Trp Trp Glu Val Asp Leu Lys Lys Met Asp Lys Val Gly Leu |     |     |
| 625                                                             | 630 | 635 |
| Val Lys Ile Tyr Asn Arg Thr Asp Ala Glu Thr Gln Arg Leu Ser Asn |     |     |
|                                                                 | 645 | 650 |
|                                                                 |     | 655 |
| Phe                                                             |     |     |

## (2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 811 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CTGTGGCAAT CAGTCAGCTG CTTCCAAACA GTCAGCTTCA GGAACGATTG AGGTGATTTT | 60  |
| ACGAGAAAAAT GGCTCTGGGA CACGGGGTGC CTTACAGAA ATCACAGGGA TTCTCAAAAA | 120 |
| AGACGGTGAT AAAAAAATTG ACAACACTGC CAAAACAGCT GTGATTCAAA ATAGTACAGA | 180 |
| AGGTGTTCTC TCAGCAGTTC AAGGGAATGC TAATGCTATC GGCTACATCT CCTTGGGATC | 240 |
| TTTAACGAAA TCTGTCAAGG CTTTAGAGAT TGATGGTGTC AAGGCTAGTC GAGACACAGT | 300 |
| TTTAGATGGT GAATACCTC TTCAACGTCC CTTCAACATT GTTTGGTCTT CTAATCTTTC  | 360 |
| CAAGCTAGGT CAAGATTTTA TCAGCTTTAT CCACTCCAAA CAAGGTCAAC AAGTGGTCAC | 420 |
| AGATAATAAA TTTATTGAAG CTAAAACCGA AACCACGGAA TATACAAGCC AACACTTATC | 480 |
| AGGCAAGTTG TCTGTTGTAG GTTCCACTTC AGTATCTTCT TTAATGGAAA AATTAGCAGA | 540 |
| AGCTTATAAA AAAGAAAATC CAGAAGTTAC GATTGATATT ACCTCTAATG GGTCTTCAGC | 600 |
| AGGTATTACC GCTGTTAAGG AGAAAACCGC TGATATTGGT ATGGTTTCTA GGAATTAAC  | 660 |
| TCCTGAAGAA GGTAAGAGTC TCACCCATGA TGCTATTGCT TTAGACGGTA TTGCTGTTGT | 720 |
| GGTCAATAAT GACAATAAGG CAAGCCAAGT CAGTATGGCT GAACTTGCAG ACGTTTTTAG | 780 |
| TGGCAAATTA ACCACCTGGG ACAAGATTAA A                                | 811 |

## (2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 270 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Cys Gly Asn Gln Ser Ala Ala Ser Lys Gln Ser Ala Ser Gly Thr Ile  
 1 5 10 15  
 Glu Val Ile Ser Arg Glu Asn Gly Ser Gly Thr Arg Gly Ala Phe Thr  
 20 25 30  
 Glu Ile Thr Gly Ile Leu Lys Lys Asp Gly Asp Lys Lys Ile Asp Asn  
 35 40 45  
 Thr Ala Lys Thr Ala Val Ile Gln Asn Ser Thr Glu Gly Val Leu Ser  
 50 55 60  
 Ala Val Gln Gly Asn Ala Asn Ala Ile Gly Tyr Ile Ser Leu Gly Ser  
 65 70 75 80  
 Leu Thr Lys Ser Val Lys Ala Leu Glu Ile Asp Gly Val Lys Ala Ser  
 85 90 95  
 Arg Asp Thr Val Leu Asp Gly Glu Tyr Pro Leu Gln Arg Pro Phe Asn  
 100 105 110  
 Ile Val Trp Ser Ser Asn Leu Ser Lys Leu Gly Gln Asp Phe Ile Ser  
 115 120 125  
 Phe Ile His Ser Lys Gln Gly Gln Gln Val Val Thr Asp Asn Lys Phe  
 130 135 140  
 Ile Glu Ala Lys Thr Glu Thr Thr Glu Tyr Thr Ser Gln His Leu Ser  
 145 150 155 160  
 Gly Lys Leu Ser Val Val Gly Ser Thr Ser Val Ser Ser Leu Met Glu  
 165 170 175  
 Lys Leu Ala Glu Ala Tyr Lys Lys Glu Asn Pro Glu Val Thr Ile Asp  
 180 185 190  
 Ile Thr Ser Asn Gly Ser Ser Ala Gly Ile Thr Ala Val Lys Glu Lys  
 195 200 205  
 Thr Ala Asp Ile Gly Met Val Ser Arg Glu Leu Thr Pro Glu Glu Gly  
 210 215 220  
 Lys Ser Leu Thr His Asp Ala Ile Ala Leu Asp Gly Ile Ala Val Val  
 225 230 235 240  
 Val Asn Asn Asp Asn Lys Ala Ser Gln Val Ser Met Ala Glu Leu Ala  
 245 250 255  
 Asp Val Phe Ser Gly Lys Leu Thr Thr Trp Asp Lys Ile Lys  
 260 265 270

## (2) INFORMATION FOR SEQ ID NO: 207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 805 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

```

TTGTCAACAA CAACATGCTA CTTCTGAGGG GACGAATCAA AGGCAAAGCA GTTCAGCGAA      60
AGTTCCATGG AAAGCTTCAT ACACCAACCT AAACAACCAG GTAAGTACAG AAGAGGTCAA      120
ATCTCTCTTA TCAGCTCACT TGGATCCAAA TAGTGTTGAT GCATTTTTTTA ATCTCGTTAA      180
TGACTATAAT ACCATTGTCTG GCTCAACTGG CTTATCAGGA GATTTCACCT CCTTTACTCA      240
CACCGAATAC GATGTTGAGA AAATCAGTCA TCTCTGGAAT CAAAAGAAGG GCGATTTTGT      300
TGGGACCAAC TGCCGTATCA ATAGTTATTG TCTTTTGAAA AATTCAGTCA CCATTCCAAA      360
GCTTGAAAAG AATGACCAGT TGCTTTTCCT AGATAATGAT GCGATTGATA AAGGAAAGGT      420
CTTTGATTCA CAAGATAAGG AAGAGTTTGA TATTCTATTT TCGAGAGTTC CAACTGAGTC      480
AACTACAGAT GTCAAGGTTT ACGCTGAAAA GATGGAAGCA TTCTTCTCAC AATTTCAATT      540
CAATGAAAAA GCTCGAATGC TGTCTGTAGT CTTGCACGAC AATTTGGATG GCGAGTATCT      600
GTTTGTAGGC CACGTTGGGG TCTTAGTACC TGCTGATGAC GGTTTCTTAT TTGTAGAGAA      660
ATTGACTTTC GAAGAGCCCT ACCAAGCGAT TAAATTTGCT AGTAAGGAAG ATTGCTACAA      720
GTATTTGGGC ACCAAGTATG CGGATTATAC AGGCGAGGGA CTGGCTAAGC CTTTATCAT      780
GGATAATGAT AAGTGGGTTA AACTT      805

```

## (2) INFORMATION FOR SEQ ID NO:208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```

Cys Gln Gln Gln His Ala Thr Ser Glu Gly Thr Asn Gln Arg Gln Ser
1          5          10          15
Ser Ser Ala Lys Val Pro Trp Lys Ala Ser Tyr Thr Asn Leu Asn Asn
20          25          30
Gln Val Ser Thr Glu Glu Val Lys Ser Leu Leu Ser Ala His Leu Asp
35          40          45
Pro Asn Ser Val Asp Ala Phe Phe Asn Leu Val Asn Asp Tyr Asn Thr
50          55          60
Ile Val Gly Ser Thr Gly Leu Ser Gly Asp Phe Thr Ser Phe Thr His
65          70          75          80
Thr Glu Tyr Asp Val Glu Lys Ile Ser His Leu Trp Asn Gln Lys Lys
85          90          95
Gly Asp Phe Val Gly Thr Asn Cys Arg Ile Asn Ser Tyr Cys Leu Leu
100          105          110

```

Lys Asn Ser Val Thr Ile Pro Lys Leu Glu Lys Asn Asp Gln Leu Leu  
                   115                  120                  125  
 Phe Leu Asp Asn Asp Ala Ile Asp Lys Gly Lys Val Phe Asp Ser Gln  
           130                  135                  140  
 Asp Lys Glu Glu Phe Asp Ile Leu Phe Ser Arg Val Pro Thr Glu Ser  
   145                  150                  155                  160  
 Thr Thr Asp Val Lys Val His Ala Glu Lys Met Glu Ala Phe Phe Ser  
                   165                  170                  175  
 Gln Phe Gln Phe Asn Glu Lys Ala Arg Met Leu Ser Val Val Leu His  
                   180                  185                  190  
 Asp Asn Leu Asp Gly Glu Tyr Leu Phe Val Gly His Val Gly Val Leu  
           195                  200                  205  
 Val Pro Ala Asp Asp Gly Phe Leu Phe Val Glu Lys Leu Thr Phe Glu  
           210                  215                  220  
 Glu Pro Tyr Gln Ala Ile Lys Phe Ala Ser Lys Glu Asp Cys Tyr Lys  
   225                  230                  235                  240  
 Tyr Leu Gly Thr Lys Tyr Ala Asp Tyr Thr Gly Glu Gly Leu Ala Lys  
                   245                  250                  255  
 Pro Phe Ile Met Asp Asn Asp Lys Trp Val Lys Leu  
                   260                  265

## (2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 508 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTGTTTCAGGC AAGTCCGTGA CTAGTGAACA CCAAACGAAA GATGAAATGA AGACGGAGCA | 60  |
| GACAGCTAGT AAAACAAGCG CAGCTAAAGG GAAAGAGGTG GCTGATTTTG AATTGATGGG  | 120 |
| AGTAGATGGC AAGACCTACC GTTTATCTGA TTACAAGGGC AAGAAAGTCT ATCTCAAATT  | 180 |
| CTGGGCTTCT TGGTGTTCCT TCTGTCTGGC TAGTCTTCCA GATACGGATG AGATTGCTAA  | 240 |
| AGAAGCTGGT GATGACTATG TGGTCTTGAC AGTAGTGTCA CCAGGACATA AGGGAGAGCA  | 300 |
| ATCTGAAGCG GACTTTAAGA ATTGGTATAA GGGATTGGAT TATAAAAATC TCCCAGTCCT  | 360 |
| AGTTGACCCA TCAGGCAAAC TTTTGAAAC TTATGGTGTC CGTTCTTACC CAACCCAAGC   | 420 |
| CTTTATAGAC AAAGAAGGCA AGCTGGTCAA AACACATCCA GGATTCATGG AAAAAGATGC  | 480 |
| AATTTTGCAA ACTTTGAAGG AATTAGCC                                     | 508 |

## (2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 169 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Cys | Ser | Gly | Lys | Ser | Val | Thr | Ser | Glu | His | Gln | Thr | Lys | Asp | Glu | Met |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Thr | Glu | Gln | Thr | Ala | Ser | Lys | Thr | Ser | Ala | Ala | Lys | Gly | Lys | Glu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Ala | Asp | Phe | Glu | Leu | Met | Gly | Val | Asp | Gly | Lys | Thr | Tyr | Arg | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Asp | Tyr | Lys | Gly | Lys | Lys | Val | Tyr | Leu | Lys | Phe | Trp | Ala | Ser | Trp |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Cys | Ser | Ile | Cys | Leu | Ala | Ser | Leu | Pro | Asp | Thr | Asp | Glu | Ile | Ala | Lys |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Glu | Ala | Gly | Asp | Asp | Tyr | Val | Val | Leu | Thr | Val | Val | Ser | Pro | Gly | His |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Lys | Gly | Glu | Gln | Ser | Glu | Ala | Asp | Phe | Lys | Asn | Trp | Tyr | Lys | Gly | Leu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asp | Tyr | Lys | Asn | Leu | Pro | Val | Leu | Val | Asp | Pro | Ser | Gly | Lys | Leu | Leu |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Glu | Thr | Tyr | Gly | Val | Arg | Ser | Tyr | Pro | Thr | Gln | Ala | Phe | Ile | Asp | Lys |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Glu | Gly | Lys | Leu | Val | Lys | Thr | His | Pro | Gly | Phe | Met | Glu | Lys | Asp | Ala |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ile | Leu | Gln | Thr | Leu | Lys | Glu | Leu | Ala |     |     |     |     |     |     |     |  |
|     |     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO: 211:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 994 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CTCGCAAATT | GAAAAGGCCG | CAGTTAGCCA | AGGAGGAAAA | GCAGTGAAAA | AAACAGAAAT | 60  |
| TAGTAAAGAC | GCAGACTTGC | ACGAAATTTA | TCTAGCTGGA | GGTTGTTTCT | GGGGAGTGGA | 120 |
| GGAATATTTT | TCACGTGTTC | CCGGGGTGAC | GGATGCCGTT | TCAGGCTATG | CAATGGTAG  | 180 |
| AGGAGAAACA | ACCAAGTACG | AATTGATTAA | CCAAACAGGT | CATGCAGAAA | CCGTCCATGT | 240 |
| CACCTATGAT | GCCAAGCAAA | TTTCTCTCAA | GGAAATCCTG | CTTCACTATT | TCCGCATTAT | 300 |

```

CAATCCAACC AGCAAAAATA AACAAGGAAA TGATGTGGGG ACCCAGTACC GTACTGGTGT      360
TTATTACACA GATGACAAGG ATTTGGAAGT GATTAACCAA GTCTTTGATG AGGTGGCTAA      420
GAAATACGAT CAACCTCTAG CAGTTGAAAA GGAAAACTTG AAGAATTTTG TGGTGGCTGA      480
GGATTACCAT CAAGACTATC TCAAGAAAAA TCCAAATGGC TACTGCCATA TCAATGTTAA      540
TCAGGCGGCC TATCCTGTCA TTGATGCCAG CAAATATCCA AAACCAAGTG ATGAGGAATT      600
GAAAAAGACC CTGTCACCTG AGGAGTATGC AGTTACCCAG GAAAATCAAA CAGAACGAGC      660
TTTCTCAAAC CGTACTGGG ATAAATTTGA ATCCGGTATC TATGTGGATA TAGCAACTGG      720
GGAACCTCTC TTTTCATCAA AAGACAAATT TGAGTCTGGT TGTGGCTGGC CTAGTTTAC      780
CCAACCCATC AGTCCAGATG TTGTCACCTA CAAGGAAGAT AAGTCCTACA ATATGACGCG      840
TATGGAAGTG CGGAGCCGAG TAGGAGATTC TCACCTTGGG CATGTCTTTA CGGATGGTCC      900
ACAGGACAAG GCGGGCTTAC GTTACTGTAT CAATAGCCTC TCTATCCGCT TTATTCCCAA      960
AGACCAAATG GAAGAAAAAG GTACGCTTAT TTAC                                  994

```

## (2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 331 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```

Ser Gln Ile Glu Lys Ala Ala Val Ser Gln Gly Gly Lys Ala Val Lys
1          5          10          15
Lys Thr Glu Ile Ser Lys Asp Ala Asp Leu His Glu Ile Tyr Leu Ala
20        25        30
Gly Gly Cys Phe Trp Gly Val Glu Glu Tyr Phe Ser Arg Val Pro Gly
35        40        45
Val Thr Asp Ala Val Ser Gly Tyr Ala Asn Gly Arg Gly Glu Thr Thr
50        55        60
Lys Tyr Glu Leu Ile Asn Gln Thr Gly His Ala Glu Thr Val His Val
65        70        75        80
Thr Tyr Asp Ala Lys Gln Ile Ser Leu Lys Glu Ile Leu Leu His Tyr
85        90        95
Phe Arg Ile Ile Asn Pro Thr Ser Lys Asn Lys Gln Gly Asn Asp Val
100       105       110
Gly Thr Gln Tyr Arg Thr Gly Val Tyr Tyr Thr Asp Asp Lys Asp Leu
115       120       125
Glu Val Ile Asn Gln Val Phe Asp Glu Val Ala Lys Lys Tyr Asp Gln
130       135       140

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Pro Leu Ala Val Glu Lys Glu Asn Leu Lys Asn Phe Val Val Ala Glu  
 145 150 155 160

Asp Tyr His Gln Asp Tyr Leu Lys Lys Asn Pro Asn Gly Tyr Cys His  
 165 170 175

Ile Asn Val Asn Gln Ala Ala Tyr Pro Val Ile Asp Ala Ser Lys Tyr  
 180 185 190

Pro Lys Pro Ser Asp Glu Glu Leu Lys Lys Thr Leu Ser Pro Glu Glu  
 195 200 205

Tyr Ala Val Thr Gln Glu Asn Gln Thr Glu Arg Ala Phe Ser Asn Arg  
 210 215 220

Tyr Trp Asp Lys Phe Glu Ser Gly Ile Tyr Val Asp Ile Ala Thr Gly  
 225 230 235 240

Glu Pro Leu Phe Ser Ser Lys Asp Lys Phe Glu Ser Gly Cys Gly Trp  
 245 250 255

Pro Ser Phe Thr Gln Pro Ile Ser Pro Asp Val Val Thr Tyr Lys Glu  
 260 265 270

Asp Lys Ser Tyr Asn Met Thr Arg Met Glu Val Arg Ser Arg Val Gly  
 275 280 285

Asp Ser His Leu Gly His Val Phe Thr Asp Gly Pro Gln Asp Lys Gly  
 290 295 300

Gly Leu Arg Tyr Cys Ile Asn Ser Leu Ser Ile Arg Phe Ile Pro Lys  
 305 310 315 320

Asp Gln Met Glu Glu Lys Gly Thr Leu Ile Tyr  
 325 330

## (2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 625 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| TTGTCAGTCA GGTTC TAATG GTTCTCAGTC TGCTGTGGAT GCTATCAAAC AAAAAGGGAA  | 60  |
| ATTAGTTGTG GCAACCAGTC CTGACTATGC ACCCTTTGAA TTTCAATCAT TGGTTGATGG   | 120 |
| AAAGAACCAG GTAGTCGGTG CAGACATCGA CATGGCTCAG GCTATCGCTG ATGAACTTGG   | 180 |
| GGTTAAGTTG GAAATCTCAA GCATGAGTTT TGACAATGTT TTGACCAGTC TTCAA ACTGG  | 240 |
| TAAGGCTGAC CTAGCAGTTG CAGGAATTAG TGCTACTGAC GAGAGAAAAG AAGTCTTTGA   | 300 |
| TTTTTCAATC CCATACTATG AAAACAAGAT TAGTTTCTTG GTTCGTAAGG CTGATGTGGA   | 360 |
| AAAATACAAG GATT TAACTA GCCTAGAAAAG TGCTAATATT GCAGCCCAAA AAGGGACTGT | 420 |
| TCCAGAATCA ATGGTCAAGG AACAAATTGCC AAAAGTTCAA TTA ACTTCCC TAACTAATAT | 480 |

GGGTGAAGCA GTCAATGAAT TGCAGGCTGG AAAAATAGAT GCTGTTCATA TGGATGAGCC 540  
 TGTTCGACTT AGTTATGCTG CTA AAAACGC TGGCTTAGCT GTCGCAACTG TCAGCTTGAA 600  
 GATGAAGGAC GGCGACGCCA ATGCC 625

## (2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 208 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Cys Gln Ser Gly Ser Asn Gly Ser Gln Ser Ala Val Asp Ala Ile Lys  
 1 5 10 15  
 Gln Lys Gly Lys Leu Val Val Ala Thr Ser Pro Asp Tyr Ala Pro Phe  
 20 25 30  
 Glu Phe Gln Ser Leu Val Asp Gly Lys Asn Gln Val Val Gly Ala Asp  
 35 40 45  
 Ile Asp Met Ala Gln Ala Ile Ala Asp Glu Leu Gly Val Lys Leu Glu  
 50 55 60  
 Ile Ser Ser Met Ser Phe Asp Asn Val Leu Thr Ser Leu Gln Thr Gly  
 65 70 75 80  
 Lys Ala Asp Leu Ala Val Ala Gly Ile Ser Ala Thr Asp Glu Arg Lys  
 85 90 95  
 Glu Val Phe Asp Phe Ser Ile Pro Tyr Tyr Glu Asn Lys Ile Ser Phe  
 100 105 110  
 Leu Val Arg Lys Ala Asp Val Glu Lys Tyr Lys Asp Leu Thr Ser Leu  
 115 120 125  
 Glu Ser Ala Asn Ile Ala Ala Gln Lys Gly Thr Val Pro Glu Ser Met  
 130 135 140  
 Val Lys Glu Gln Leu Pro Lys Val Gln Leu Thr Ser Leu Thr Asn Met  
 145 150 155 160  
 Gly Glu Ala Val Asn Glu Leu Gln Ala Gly Lys Ile Asp Ala Val His  
 165 170 175  
 Met Asp Glu Pro Val Ala Leu Ser Tyr Ala Ala Lys Asn Ala Gly Leu  
 180 185 190  
 Ala Val Ala Thr Val Ser Leu Lys Met Lys Asp Gly Asp Ala Asn Ala  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO: 215:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3022 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GGAAACTTCA CAGGATTTTA AAGAGAAGAA AACAGCAGTC ATTAAGGAAA AAGAAGTTGT  | 60   |
| TAGTAAAAAT CCTGTGATAG ACAATAACAC TAGCAATGAA GAAGCAAAAA TCAAAGAAGA  | 120  |
| AAATTCCAAT AAATCCCAAG GAGATTATAC GGACTCATTT GTGAATAAAA ACACAGAAAA  | 180  |
| TCCCAAAAAA GAAGATAAAG TTGTCTATAT TGCTGAATTT AAAGATAAAG AATCTGGAGA  | 240  |
| AAAAGCAATC AAGGAACTAT CCAGTCTTAA GAATACAAAA GTTTTATATA CTTATGATAG  | 300  |
| AATTTTAAAC GGTAGTGCCA TAGAAACAAC TCCAGATAAC TTGGACAAAA TTAAACAAAT  | 360  |
| AGAAGGTATT TCATCGGTTG AAAGGGCACA AAAAGTCCAA CCCATGATGA ATCATGCCAG  | 420  |
| AAAGGAAATT GGAGTTGAGG AAGCTATTGA TTACCTAAAG TCTATCAATG CTCCGTTTGG  | 480  |
| GAAAAATTTT GATGGTAGAG GTATGGTCAT TTCAAATATC GATACTGGAA CAGATTATAG  | 540  |
| ACATAAGGCT ATGAGAATCG ATGATGATGC CAAAGCCTCA ATGAGATTTA AAAAAGAAGA  | 600  |
| CTTAAAAGGC ACTGATAAAA ATTATTGGTT GAGTGATAAA ATCCCTCATG CGTTCAATTA  | 660  |
| TTATAATGGT GGCAAAATCA CTGTAGAAAA ATATGATGAT GGAAGGGATT ATTTTGACCC  | 720  |
| ACATGGGATG CATATTGCAG GGATTCTTGC TGGAAATGAT ACTGAACAAG ACATCAAAAA  | 780  |
| CTTTAACGGC ATAGATGGAA TTGCACCTAA TGCACAAATT TTCTCTTACA AAATGTATTC  | 840  |
| TGACGCAGGA TCTGGGTTTG CGGGTGATGA AACAAATGTTT CATGCTATTG AAGATTCTAT | 900  |
| CAAACACAAC GTTGATGTTG TTTCGGTATC ATCTGGTTTT ACAGGAACAG GTCTTGTAGG  | 960  |
| TGAGAAATAT TGGCAAGCTA TTCGGGCATT AAGAAAAGCA GGCATTCCAA TGGTTGTTCG  | 1020 |
| TACGGGTAAC TATGCGACTT CTGCTTCAAG TTCTTCATGG GATTTAGTAG CAAATAATCA  | 1080 |
| TCTGAAAATG ACCGACACTG GAAATGTAAC ACGAACTGCA GCACATGAAG ATGCGATAGC  | 1140 |
| GGTCGCTTCT GCTAAAAATC AAACAGTTGA GTTTGATAAA GTTAACATAG GTGGAGAAAG  | 1200 |
| TTTTAAATAC AGAAATATAG GGGCCTTTTT CGATAAGAGT AAAATCACAA CAAATGAAGA  | 1260 |
| TGGAACAAAA GCTCCTAGTA AATTAAAATT TGTATATATA GGCAAGGGGC AAGACCAAGA  | 1320 |
| TTTGATAGGT TTGGATCTTA GGGGCAAAAT TGCAGTAATG GATAGAATTT ATACAAAGGA  | 1380 |
| TTTAAAAAAT GCTTTTAAAA AAGCTATGGA TAAGGGTGCA CGCGCCATTA TGGTTGTAAA  | 1440 |
| TACTGTAAAT TACTACAATA GAGATAATTG GACAGAGCTT CCAGCTATGG GATATGAAGC  | 1500 |
| GGATGAAGGT ACTAAAAGTC AAGTGTTTTT AATTTTCAGGA GATGATGGTG TAAAGCTATG | 1560 |
| GAACATGATT AATCCTGATA AAAAACTGA AGTCAAAAGA AATAATAAAG AAGATTTTAA   | 1620 |
| AGATAAATTG GAGCAATACT ATCCAATTGA TATGGAAAGT TTTAATTCCA ACAAACCGAA  | 1680 |
| TGTAGGTGAC GAAAAAGAGA TTGACTTTAA GTTTGCACCT GACACAGACA AAGAACTCTA  | 1740 |

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TAAAGAAGAT ATCATCGTTC CAGCAGGATC TACATCTTGG GGGCCAAGAA TAGATTTACT      1800
TTTAAAACCC GATGTTTCAG CACCTGGTAA AAATATTAAA TCCACGCTTA ATGTTATTAA      1860
TGGCAAATCA ACTTATGGCT ATATGTCAGG AACTAGTATG GCGACTCCAA TCGTGGCAGC      1920
TTCTACTGTT TTGATTAGAC CGAAATTAAA GGAAATGCTT GAAAGACCTG TATTGAAAAA      1980
TCTTAAGGGA GATGACAAAA TAGATCTTAC AAGTCTTACA AAAATTGCCC TACAAAATAC      2040
TGCGCGACCT ATGATGGATG CAACTTCTTG GAAAGAAAAA AGTCAATACT TTGCATCACC      2100
TAGACAACAG GGAGCAGGCC TAATTAATGT GGCCAATGCT TTGAGAAATG AAGTTGTAGC      2160
AACTTTCAAA AACACTGATT CTAAAGGTTT GGTAAGTCA TATGGTTCCA TTTCTCTTAA      2220
AGAAATAAAA GGTGATAAAA AATACTTTAC AATCAAGCTT CACAATACAT CAAACAGACC      2280
TTTGACTTTT AAAGTTTCAG CATCAGCGAT AACTACAGAT TCTCTAACTG ACAGATTAAA      2340
ACTTGATGAA ACATATAAAG ATGAAAAATC TCCAGATGGT AAGCAAATTG TTCCAGAAAT      2400
TCACCCAGAA AAAGTCAAAG GAGCAAATAT CACATTTGAG CATGATACTT TCACTATAGG      2460
CGCAAATTCT AGCTTTGATT TGAATGCGGT TATAAATGTT GGAGAGGCCA AAAACAAAAA      2520
TAAATTTGTA GAATCATTTA TTCATTTTGA GTCAGTGGA GCGATGGAAG CTCTAAACTC      2580
CAGCGGGAAG AAAATAAACT TCCAACCTTC TTTGTGATG CCTCTAATGG GATTTGCTGG      2640
GAATTGGAAC CACGAACCAA TCCTTGATAA ATGGGCTTGG GAAGAAGGGT CAAGATCAAA      2700
AACACTGGGA GGTATGATG ATGATGGTAA ACCGAAAATT CCAGGAACCT TAAATAAGGG      2760
AATTGGTGGA GAACATGGTA TAGATAAATT TAATCCAGCA GGAGTTATAC AAAATAGAAA      2820
AGATAAAAAT ACAACATCCC TGGATCAAAA TCCAGAATTA TTTGCTTTCA ATAACGAAGG      2880
GATCAACGCT CCATCATCAA GTGGTTCTAA GATTGCTAAC ATTTATCCTT TAGATTCAAA      2940
TGGAAATCCT CAAGATGCTC AACTTGAAAG AGGATTAACA CCTTCTCCAC TTGTATTAAG      3000
AAGTGCAGAA GAAGGATTGA TT  3022

```

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```

Glu Thr Ser Gln Asp Phe Lys Glu Lys Lys Thr Ala Val Ile Lys Glu
1          5          10          15
Lys Glu Val Val Ser Lys Asn Pro Val Ile Asp Asn Asn Thr Ser Asn
          20          25          30
Glu Glu Ala Lys Ile Lys Glu Glu Asn Ser Asn Lys Ser Gln Gly Asp

```

| 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Thr | Asp | Ser | Phe | Val | Asn | Lys | Asn | Thr | Glu | Asn | Pro | Lys | Lys | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Lys | Val | Val | Tyr | Ile | Ala | Glu | Phe | Lys | Asp | Lys | Glu | Ser | Gly | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Ala | Ile | Lys | Glu | Leu | Ser | Ser | Leu | Lys | Asn | Thr | Lys | Val | Leu | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Tyr | Asp | Arg | Ile | Phe | Asn | Gly | Ser | Ala | Ile | Glu | Thr | Thr | Pro | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Leu | Asp | Lys | Ile | Lys | Gln | Ile | Glu | Gly | Ile | Ser | Ser | Val | Glu | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Gln | Lys | Val | Gln | Pro | Met | Met | Asn | His | Ala | Arg | Lys | Glu | Ile | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Glu | Glu | Ala | Ile | Asp | Tyr | Leu | Lys | Ser | Ile | Asn | Ala | Pro | Phe | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Asn | Phe | Asp | Gly | Arg | Gly | Met | Val | Ile | Ser | Asn | Ile | Asp | Thr | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Thr | Asp | Tyr | Arg | His | Lys | Ala | Met | Arg | Ile | Asp | Asp | Asp | Ala | Lys | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Met | Arg | Phe | Lys | Lys | Glu | Asp | Leu | Lys | Gly | Thr | Asp | Lys | Asn | Tyr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Trp | Leu | Ser | Asp | Lys | Ile | Pro | His | Ala | Phe | Asn | Tyr | Tyr | Asn | Gly | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Ile | Thr | Val | Glu | Lys | Tyr | Asp | Asp | Gly | Arg | Asp | Tyr | Phe | Asp | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| His | Gly | Met | His | Ile | Ala | Gly | Ile | Leu | Ala | Gly | Asn | Asp | Thr | Glu | Gln |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asp | Ile | Lys | Asn | Phe | Asn | Gly | Ile | Asp | Gly | Ile | Ala | Pro | Asn | Ala | Gln |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ile | Phe | Ser | Tyr | Lys | Met | Tyr | Ser | Asp | Ala | Gly | Ser | Gly | Phe | Ala | Gly |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Glu | Thr | Met | Phe | His | Ala | Ile | Glu | Asp | Ser | Ile | Lys | His | Asn | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Val | Val | Ser | Val | Ser | Ser | Gly | Phe | Thr | Gly | Thr | Gly | Leu | Val | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Glu | Lys | Tyr | Trp | Gln | Ala | Ile | Arg | Ala | Leu | Arg | Lys | Ala | Gly | Ile | Pro |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Met | Val | Val | Ala | Thr | Gly | Asn | Tyr | Ala | Thr | Ser | Ala | Ser | Ser | Ser | Ser |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Trp | Asp | Leu | Val | Ala | Asn | Asn | His | Leu | Lys | Met | Thr | Asp | Thr | Gly | Asn |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Val | Thr | Arg | Thr | Ala | Ala | His | Glu | Asp | Ala | Ile | Ala | Val | Ala | Ser | Ala |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |

Lys Asn Gln Thr Val Glu Phe Asp Lys Val Asn Ile Gly Gly Glu Ser  
 385 390 395 400  
 Phe Lys Tyr Arg Asn Ile Gly Ala Phe Phe Asp Lys Ser Lys Ile Thr  
 405 410 415  
 Thr Asn Glu Asp Gly Thr Lys Ala Pro Ser Lys Leu Lys Phe Val Tyr  
 420 425 430  
 Ile Gly Lys Gly Gln Asp Gln Asp Leu Ile Gly Leu Asp Leu Arg Gly  
 435 440 445  
 Lys Ile Ala Val Met Asp Arg Ile Tyr Thr Lys Asp Leu Lys Asn Ala  
 450 455 460  
 Phe Lys Lys Ala Met Asp Lys Gly Ala Arg Ala Ile Met Val Val Asn  
 465 470 475 480  
 Thr Val Asn Tyr Tyr Asn Arg Asp Asn Trp Thr Glu Leu Pro Ala Met  
 485 490 495  
 Gly Tyr Glu Ala Asp Glu Gly Thr Lys Ser Gln Val Phe Ser Ile Ser  
 500 505 510  
 Gly Asp Asp Gly Val Lys Leu Trp Asn Met Ile Asn Pro Asp Lys Lys  
 515 520 525  
 Thr Glu Val Lys Arg Asn Asn Lys Glu Asp Phe Lys Asp Lys Leu Glu  
 530 535 540  
 Gln Tyr Tyr Pro Ile Asp Met Glu Ser Phe Asn Ser Asn Lys Pro Asn  
 545 550 555 560  
 Val Gly Asp Glu Lys Glu Ile Asp Phe Lys Phe Ala Pro Asp Thr Asp  
 565 570 575  
 Lys Glu Leu Tyr Lys Glu Asp Ile Ile Val Pro Ala Gly Ser Thr Ser  
 580 585 590  
 Trp Gly Pro Arg Ile Asp Leu Leu Leu Lys Pro Asp Val Ser Ala Pro  
 595 600 605  
 Gly Lys Asn Ile Lys Ser Thr Leu Asn Val Ile Asn Gly Lys Ser Thr  
 610 615 620  
 Tyr Gly Tyr Met Ser Gly Thr Ser Met Ala Thr Pro Ile Val Ala Ala  
 625 630 635 640  
 Ser Thr Val Leu Ile Arg Pro Lys Leu Lys Glu Met Leu Glu Arg Pro  
 645 650 655  
 Val Leu Lys Asn Leu Lys Gly Asp Asp Lys Ile Asp Leu Thr Ser Leu  
 660 665 670  
 Thr Lys Ile Ala Leu Gln Asn Thr Ala Arg Pro Met Met Asp Ala Thr  
 675 680 685  
 Ser Trp Lys Glu Lys Ser Gln Tyr Phe Ala Ser Pro Arg Gln Gln Gly  
 690 695 700  
 Ala Gly Leu Ile Asn Val Ala Asn Ala Leu Arg Asn Glu Val Val Ala  
 705 710 715 720

Thr Phe Lys Asn Thr Asp Ser Lys Gly Leu Val Asn Ser Tyr Gly Ser  
 725 730 735  
 Ile Ser Leu Lys Glu Ile Lys Gly Asp Lys Lys Tyr Phe Thr Ile Lys  
 740 745 750  
 Leu His Asn Thr Ser Asn Arg Pro Leu Thr Phe Lys Val Ser Ala Ser  
 755 760 765  
 Ala Ile Thr Thr Asp Ser Leu Thr Asp Arg Leu Lys Leu Asp Glu Thr  
 770 775 780  
 Tyr Lys Asp Glu Lys Ser Pro Asp Gly Lys Gln Ile Val Pro Glu Ile  
 785 790 795 800  
 His Pro Glu Lys Val Lys Gly Ala Asn Ile Thr Phe Glu His Asp Thr  
 805 810 815  
 Phe Thr Ile Gly Ala Asn Ser Ser Phe Asp Leu Asn Ala Val Ile Asn  
 820 825 830  
 Val Gly Glu Ala Lys Asn Lys Asn Lys Phe Val Glu Ser Phe Ile His  
 835 840 845  
 Phe Glu Ser Val Glu Ala Met Glu Ala Leu Asn Ser Ser Gly Lys Lys  
 850 855 860  
 Ile Asn Phe Gln Pro Ser Leu Ser Met Pro Leu Met Gly Phe Ala Gly  
 865 870 875 880  
 Asn Trp Asn His Glu Pro Ile Leu Asp Lys Trp Ala Trp Glu Glu Gly  
 885 890 895  
 Ser Arg Ser Lys Thr Leu Gly Gly Tyr Asp Asp Asp Gly Lys Pro Lys  
 900 905 910  
 Ile Pro Gly Thr Leu Asn Lys Gly Ile Gly Gly Glu His Gly Ile Asp  
 915 920 925  
 Lys Phe Asn Pro Ala Gly Val Ile Gln Asn Arg Lys Asp Lys Asn Thr  
 930 935 940  
 Thr Ser Leu Asp Gln Asn Pro Glu Leu Phe Ala Phe Asn Asn Glu Gly  
 945 950 955 960  
 Ile Asn Ala Pro Ser Ser Ser Gly Ser Lys Ile Ala Asn Ile Tyr Pro  
 965 970 975  
 Leu Asp Ser Asn Gly Asn Pro Gln Asp Ala Gln Leu Glu Arg Gly Leu  
 980 985 990  
 Thr Pro Ser Pro Leu Val Leu Arg Ser Ala Glu Glu Gly Leu Ile  
 995 1000 1005

## (2) INFORMATION FOR SEQ ID NO: 217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1696 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TGTGGTCGAA GTTGAGACTC CTCAATCAAT AACAAATCAG GAGCAAGCTA GGACAGAAAA  | 60   |
| CCAAGTAGTA GAGACAGAGG AAGCTCCAAA AGAAGAAGCA CCTAAAACAG AAGAAAGTCC  | 120  |
| AAAGGAAGAA CCAAAATCGG AGGTAAAACC TACTGACGAC ACCCTTCCTA AAGTAGAAGA  | 180  |
| GGGGAAAGAA GATTTCAGCAG AACCAGCTCC AGTTGAAGAA GTAGGTGGAG AAGTTGAGTC | 240  |
| AAAACCAGAG GAAAAAGTAG CAGTTAAGCC AGAAAGTCAA CCATCAGACA AACCAGCTGA  | 300  |
| GGAATCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AAAAGGCACC  | 360  |
| AGTCGAGCCA GAAAAGCAAC CAGAAGCTCC TGAAGAAGAG AAGGCTGTAG AGGAAACACC  | 420  |
| GAAACAAGAA GAGTCAACTC CAGATACCAA GGCTGAAGAA ACTGTAGAAC CAAAAGAGGA  | 480  |
| GACTGTTAAT CAATCTATTG AACAAACCAA AGTTGAAACG CCTGCTGTAG AAAACAAAC   | 540  |
| AGAACCAACA GAGGAACCAA AAGTTGAACA AGCAGGTGAA CCAGTCGCGC CAAGAGAAGA  | 600  |
| CGAACAGGCA CCAACGGCAC CAGTTGAGCC AGAAAAGCAA CCAGAAAGTTC CTGAAGAAGA | 660  |
| GAAGGCTGTA GAGGAAACAC CGAAACCAGA AGATAAAATA AAGGGTATTG GTACTAAAGA  | 720  |
| ACCAGTTGAT AAAAGTGAGT TAAATAATCA AATTGATAAA GCTAGTTCAG TTTCTCCTAC  | 780  |
| TGATTATTCT ACAGCAAGTT ACAATGCTCT TGGACCTGTT TTAGAAACTG CAAAAGGTGT  | 840  |
| CTATGCTTCA GAGCCTGTAA AACAGCCTGA GGTAAATAGC GAGACAAATA AACTTAAAC   | 900  |
| GGCTATTGAC GCTCTAAACG TTGATAAAAC TGAATTAAAC AATACGATTG CAGATGCAAA  | 960  |
| AACAAAGGTA AAAGAACATT ACAGTGATAG AAGTTGGCAA AACCTCCAAA CTGAAGTTAC  | 1020 |
| AAAGGCTGAA AAAGTTGCAG CTAATACAGA TGCTAAACAA AGTGAAGTTA ACGAAGCTGT  | 1080 |
| TGAAAAATTA ACTGCAACTA TTGAAAAATT GGTTGAATTA TCTGAAAAGC CAATATTAAC  | 1140 |
| ATTGACTAGT ACCGATAAGA AAATATTGGA ACGTGAAGCT GTTGCTAAGT ATACTCTAGA  | 1200 |
| AAATCAAAAC AAAACAAAAA TCAAATCAAT CACAGCTGAA TTGAAAAAG GAGAAGAAGT   | 1260 |
| TATTAATACT GTAGTCCTTA CAGATGACAA GGTAACAACA GAAACTATAA GCGCTGCATT  | 1320 |
| TAAGAACCTA GAGTACTACA AAGAATACAC CCTATCTACA ACTATGATTT ACGACAGAGG  | 1380 |
| TAACGGTGAA GAAACTGAAA CTCTAGAAAA TCAAAATATT CAATTAGATC TTAAAAAGT   | 1440 |
| TGAGCTTAAA AATATTAAAC GTACAGATTT AATCAAATAC GAAAATGGAA AAGAACTAA   | 1500 |
| TGAATCACTG ATAACAATA TTCCTGATGA TAAGAGCAAT TATTATTAA AAATAACTTC    | 1560 |
| AAATAATCAG AAAACTACAT TACTAGCTGT TAAAAATATA GAAGAACTA CGGTTAACGG   | 1620 |
| AACACCTGTA TATAAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA  | 1680 |
| TAAATTTGAA GAAGAA                                                  | 1696 |

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 565 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Glu | Val | Glu | Thr | Pro | Gln | Ser | Ile | Thr | Asn | Gln | Glu | Gln | Ala | 1   | 5   | 10  | 15  |
| Arg | Thr | Glu | Asn | Gln | Val | Val | Glu | Thr | Glu | Glu | Ala | Pro | Lys | Glu | Glu | 20  | 25  | 30  |     |
| Ala | Pro | Lys | Thr | Glu | Glu | Ser | Pro | Lys | Glu | Glu | Pro | Lys | Ser | Glu | Val | 35  | 40  | 45  |     |
| Lys | Pro | Thr | Asp | Asp | Thr | Leu | Pro | Lys | Val | Glu | Glu | Gly | Lys | Glu | Asp | 50  | 55  | 60  |     |
| Ser | Ala | Glu | Pro | Ala | Pro | Val | Glu | Glu | Val | Gly | Gly | Glu | Val | Glu | Ser | 65  | 70  | 75  | 80  |
| Lys | Pro | Glu | Glu | Lys | Val | Ala | Val | Lys | Pro | Glu | Ser | Gln | Pro | Ser | Asp | 85  | 90  | 95  |     |
| Lys | Pro | Ala | Glu | Glu | Ser | Lys | Val | Glu | Gln | Ala | Gly | Glu | Pro | Val | Ala | 100 | 105 | 110 |     |
| Pro | Arg | Glu | Asp | Glu | Lys | Ala | Pro | Val | Glu | Pro | Glu | Lys | Gln | Pro | Glu | 115 | 120 | 125 |     |
| Ala | Pro | Glu | Glu | Glu | Lys | Ala | Val | Glu | Glu | Thr | Pro | Lys | Gln | Glu | Glu | 130 | 135 | 140 |     |
| Ser | Thr | Pro | Asp | Thr | Lys | Ala | Glu | Glu | Thr | Val | Glu | Pro | Lys | Glu | Glu | 145 | 150 | 155 | 160 |
| Thr | Val | Asn | Gln | Ser | Ile | Glu | Gln | Pro | Lys | Val | Glu | Thr | Pro | Ala | Val | 165 | 170 | 175 |     |
| Glu | Lys | Gln | Thr | Glu | Pro | Thr | Glu | Glu | Pro | Lys | Val | Glu | Gln | Ala | Gly | 180 | 185 | 190 |     |
| Glu | Pro | Val | Ala | Pro | Arg | Glu | Asp | Glu | Gln | Ala | Pro | Thr | Ala | Pro | Val | 195 | 200 | 205 |     |
| Glu | Pro | Glu | Lys | Gln | Pro | Glu | Val | Pro | Glu | Glu | Glu | Lys | Ala | Val | Glu | 210 | 215 | 220 |     |
| Glu | Thr | Pro | Lys | Pro | Glu | Asp | Lys | Ile | Lys | Gly | Ile | Gly | Thr | Lys | Glu | 225 | 230 | 235 | 240 |
| Pro | Val | Asp | Lys | Ser | Glu | Leu | Asn | Asn | Gln | Ile | Asp | Lys | Ala | Ser | Ser | 245 | 250 | 255 |     |
| Val | Ser | Pro | Thr | Asp | Tyr | Ser | Thr | Ala | Ser | Tyr | Asn | Ala | Leu | Gly | Pro | 260 | 265 | 270 |     |
| Val | Leu | Glu | Thr | Ala | Lys | Gly | Val | Tyr | Ala | Ser | Glu | Pro | Val | Lys | Gln | 275 | 280 | 285 |     |
| Pro | Glu | Val | Asn | Ser | Glu | Thr | Asn | Lys | Leu | Lys | Thr | Ala | Ile | Asp | Ala |     |     |     |     |

| 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Val | Asp | Lys | Thr | Glu | Leu | Asn | Asn | Thr | Ile | Ala | Asp | Ala | Lys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr | Lys | Val | Lys | Glu | His | Tyr | Ser | Asp | Arg | Ser | Trp | Gln | Asn | Leu | Gln |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Thr | Glu | Val | Thr | Lys | Ala | Glu | Lys | Val | Ala | Ala | Asn | Thr | Asp | Ala | Lys |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gln | Ser | Glu | Val | Asn | Glu | Ala | Val | Glu | Lys | Leu | Thr | Ala | Thr | Ile | Glu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Lys | Leu | Val | Glu | Leu | Ser | Glu | Lys | Pro | Ile | Leu | Thr | Leu | Thr | Ser | Thr |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Asp | Lys | Lys | Ile | Leu | Glu | Arg | Glu | Ala | Val | Ala | Lys | Tyr | Thr | Leu | Glu |
| 385 |     |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |
| Asn | Gln | Asn | Lys | Thr | Lys | Ile | Lys | Ser | Ile | Thr | Ala | Glu | Leu | Lys | Lys |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Gly | Glu | Glu | Val | Ile | Asn | Thr | Val | Val | Leu | Thr | Asp | Asp | Lys | Val | Thr |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Thr | Glu | Thr | Ile | Ser | Ala | Ala | Phe | Lys | Asn | Leu | Glu | Tyr | Tyr | Lys | Glu |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Tyr | Thr | Leu | Ser | Thr | Thr | Met | Ile | Tyr | Asp | Arg | Gly | Asn | Gly | Glu | Glu |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Thr | Glu | Thr | Leu | Glu | Asn | Gln | Asn | Ile | Gln | Leu | Asp | Leu | Lys | Lys | Val |
| 465 |     |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     | 480 |
| Glu | Leu | Lys | Asn | Ile | Lys | Arg | Thr | Asp | Leu | Ile | Lys | Tyr | Glu | Asn | Gly |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Lys | Glu | Thr | Asn | Glu | Ser | Leu | Ile | Thr | Thr | Ile | Pro | Asp | Asp | Lys | Ser |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Asn | Tyr | Tyr | Leu | Lys | Ile | Thr | Ser | Asn | Asn | Gln | Lys | Thr | Thr | Leu | Leu |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Ala | Val | Lys | Asn | Ile | Glu | Glu | Thr | Thr | Val | Asn | Gly | Thr | Pro | Val | Tyr |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Lys | Val | Thr | Ala | Ile | Ala | Asp | Asn | Leu | Val | Ser | Arg | Thr | Ala | Asp | Asn |
| 545 |     |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     | 560 |
| Lys | Phe | Glu | Glu | Glu |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 565 |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 219:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1879 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| AACACCTGTA TATAAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA  | 60   |
| TAAATTTGAA GAAGAATACG TTCACTATAT TGAAAAACCT AAAGTCCACG AAGATAATGT  | 120  |
| ATATTATAAT TTCAAAGAAT TAGTGGAAGC TATTCAAAAC GATCCTTCAA AAGAATATCG  | 180  |
| TCTGGGACAA TCAATGAGCG CTAGAAATGT TGTTCCTAAT GGAAAATCAT ATATCACTAA  | 240  |
| AGAATTCACA GGAAACTTT TAAGTTCTGA AGGAAAACAA TTTGCTATTA CTGAATTGGA   | 300  |
| ACATCCATTA TTTAATGTGA TAACAAACGC AACGATAAAT AATGTGAATT TTGAAAATGT  | 360  |
| AGAGATAGAA CGTTCTGGTC AAGATAATAT TGCATCATT GCCAATACTA TGAAAGGTTT   | 420  |
| TTCAGTTATT ACAAATGTCA AAATTACAGG CACACTTTCA GGTTCGTAATA ATGTTGCTGG | 480  |
| ATTTGTAAAT AATATGAATG ATGGAACCTG TATTGAAAAT GTTGCTTTCT TTGGCAAAC   | 540  |
| ACACTCTACA AGTGGAATG GCTCTCATA AGGGGGAATT GCAGGTACAA ACTATAGAGG    | 600  |
| AATTGTTAGA AAAGCATATG TTGATGCTAC TATTACAGGA AACAAAACAC GCGCCAGCTT  | 660  |
| GTTAGTTCCT AAAGTAGATT ATGGATTAAC TCTAGACCAT CTTATTGGTA CAAAAGCTCT  | 720  |
| CCTAACTGAG TCGGTTGTAA AAGGTAAAAT AGATGTTTCA AATCCAGTAG AAGTTGGAGC  | 780  |
| AATAGCAAGT AAGACTTGGC CTGTAGGTAC GGTAAGTAAT TCTGTCAGCT ATGCTAAGAT  | 840  |
| TATCCGTGGA GAGGAGTTAT TCGGCTCTAA CGACGTTGAT GATTCTGATT ATGCTAGTGC  | 900  |
| TCATATAAAA GATTTATATG CGGTAGAGGG ATATTCGTCA GGTAATAGAT CATTTAGGAA  | 960  |
| ATCTAAAACA TTTACTAAAT TAACTAAAGA ACAAGCTGAT GCTAAAGTTA CTACTTTCAA  | 1020 |
| TATTACTGCT GATAAATTAG AAAGTGATCT ATCTCCTCTT GCAAACTTA ATGAAGAAAA   | 1080 |
| AGCCTATTCT AGTATTCAAG ATTATAACGC TGAATATAAC CAAGCCTATA AAAATCTTGA  | 1140 |
| AAAATTAATA CCATTCTACA ATAAAGATTA TATTGTATAT CAAGGTAATA AATTAAATAA  | 1200 |
| AGAACACCAT CTAAATACTA AAGAAGTTCT TTCTGTTACC GCGATGAACA ACAATGAGTT  | 1260 |
| TATCACAAAC CTAGATGAAG CTAATAAAAT TATTGTTTAC TATGCGGACG GTACAAAAGA  | 1320 |
| TTACTTTAAC TTGTCTTCTA GCAGTGAAGG TTTAAGTAAT GTAAAAGAAT ATACTATAAC  | 1380 |
| TGACTTAGGA ATTAAATATA CACCTAATAT CGTTCAAAAA GATAACACTA CTCTTGTTAA  | 1440 |
| TGATATAAAA TCTATTTTAG AATCAGTAGA GCTTCAGTCT CAAACGATGT ATCAGCATCT  | 1500 |
| AAATCGATTA GGTGACTATA GAGTTAATGC AATCAAAGAT TTATATTTAG AAGAAAGCTT  | 1560 |
| CACAGATGTT AAAGAAAAC TAACAAACCT AATCACAAAA TTAGTTCAAA ACGAAGAACA   | 1620 |
| TCAACTAAAT GATTCTCCAG CTGCTCGTCA AATGATTTCG GATAAAGTCG AGAAAAACAA  | 1680 |
| AGCAGCTTTA TTACTAGGTT TAACTTACCT AAATCGTTAC TATGGAGTTA AATTTGGTGA  | 1740 |
| TGTTAATATT AAAGAATTAA TGCTATTCAA ACCAGATTTT TATGGTGAAA AAGTTAGCGT  | 1800 |
| ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT  | 1860 |
| CGACGCATTC GGTCAAGTA                                               | 1879 |

## (2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 626 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

```

Thr Pro Val Tyr Lys Val Thr Ala Ile Ala Asp Asn Leu Val Ser Arg
1          5          10          15
Thr Ala Asp Asn Lys Phe Glu Glu Glu Tyr Val His Tyr Ile Glu Lys
20          25          30
Pro Lys Val His Glu Asp Asn Val Tyr Tyr Asn Phe Lys Glu Leu Val
35          40          45
Glu Ala Ile Gln Asn Asp Pro Ser Lys Glu Tyr Arg Leu Gly Gln Ser
50          55          60
Met Ser Ala Arg Asn Val Val Pro Asn Gly Lys Ser Tyr Ile Thr Lys
65          70          75          80
Glu Phe Thr Gly Lys Leu Leu Ser Ser Glu Gly Lys Gln Phe Ala Ile
85          90          95
Thr Glu Leu Glu His Pro Leu Phe Asn Val Ile Thr Asn Ala Thr Ile
100         105         110
Asn Asn Val Asn Phe Glu Asn Val Glu Ile Glu Arg Ser Gly Gln Asp
115         120         125
Asn Ile Ala Ser Leu Ala Asn Thr Met Lys Gly Ser Ser Val Ile Thr
130         135         140
Asn Val Lys Ile Thr Gly Thr Leu Ser Gly Arg Asn Asn Val Ala Gly
145         150         155         160
Phe Val Asn Asn Met Asn Asp Gly Thr Arg Ile Glu Asn Val Ala Phe
165         170         175
Phe Gly Lys Leu His Ser Thr Ser Gly Asn Gly Ser His Thr Gly Gly
180         185         190
Ile Ala Gly Thr Asn Tyr Arg Gly Ile Val Arg Lys Ala Tyr Val Asp
195         200         205
Ala Thr Ile Thr Gly Asn Lys Thr Arg Ala Ser Leu Leu Val Pro Lys
210         215         220
Val Asp Tyr Gly Leu Thr Leu Asp His Leu Ile Gly Thr Lys Ala Leu
225         230         235         240
Leu Thr Glu Ser Val Val Lys Gly Lys Ile Asp Val Ser Asn Pro Val
245         250         255
Glu Val Gly Ala Ile Ala Ser Lys Thr Trp Pro Val Gly Thr Val Ser
260         265         270

```

Asn Ser Val Ser Tyr Ala Lys Ile Ile Arg Gly Glu Glu Leu Phe Gly  
 275 280 285  
 Ser Asn Asp Val Asp Asp Ser Asp Tyr Ala Ser Ala His Ile Lys Asp  
 290 295 300  
 Leu Tyr Ala Val Glu Gly Tyr Ser Ser Gly Asn Arg Ser Phe Arg Lys  
 305 310 315 320  
 Ser Lys Thr Phe Thr Lys Leu Thr Lys Glu Gln Ala Asp Ala Lys Val  
 325 330 335  
 Thr Thr Phe Asn Ile Thr Ala Asp Lys Leu Glu Ser Asp Leu Ser Pro  
 340 345 350  
 Leu Ala Lys Leu Asn Glu Glu Lys Ala Tyr Ser Ser Ile Gln Asp Tyr  
 355 360 365  
 Asn Ala Glu Tyr Asn Gln Ala Tyr Lys Asn Leu Glu Lys Leu Ile Pro  
 370 375 380  
 Phe Tyr Asn Lys Asp Tyr Ile Val Tyr Gln Gly Asn Lys Leu Asn Lys  
 385 390 395 400  
 Glu His His Leu Asn Thr Lys Glu Val Leu Ser Val Thr Ala Met Asn  
 405 410 415  
 Asn Asn Glu Phe Ile Thr Asn Leu Asp Glu Ala Asn Lys Ile Ile Val  
 420 425 430  
 His Tyr Ala Asp Gly Thr Lys Asp Tyr Phe Asn Leu Ser Ser Ser Ser  
 435 440 445  
 Glu Gly Leu Ser Asn Val Lys Glu Tyr Thr Ile Thr Asp Leu Gly Ile  
 450 455 460  
 Lys Tyr Thr Pro Asn Ile Val Gln Lys Asp Asn Thr Thr Leu Val Asn  
 465 470 475 480  
 Asp Ile Lys Ser Ile Leu Glu Ser Val Glu Leu Gln Ser Gln Thr Met  
 485 490 495  
 Tyr Gln His Leu Asn Arg Leu Gly Asp Tyr Arg Val Asn Ala Ile Lys  
 500 505 510  
 Asp Leu Tyr Leu Glu Glu Ser Phe Thr Asp Val Lys Glu Asn Leu Thr  
 515 520 525  
 Asn Leu Ile Thr Lys Leu Val Gln Asn Glu Glu His Gln Leu Asn Asp  
 530 535 540  
 Ser Pro Ala Ala Arg Gln Met Ile Arg Asp Lys Val Glu Lys Asn Lys  
 545 550 555 560  
 Ala Ala Leu Leu Leu Gly Leu Thr Tyr Leu Asn Arg Tyr Tyr Gly Val  
 565 570 575  
 Lys Phe Gly Asp Val Asn Ile Lys Glu Leu Met Leu Phe Lys Pro Asp  
 580 585 590  
 Phe Tyr Gly Glu Lys Val Ser Val Leu Asp Arg Leu Ile Glu Ile Gly  
 595 600 605

Ser Lys Glu Asn Asn Ile Lys Gly Ser Arg Thr Phe Asp Ala Phe Gly  
 610 615 620  
 Gln Val  
 625

## (2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1777 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT | 60   |
| CGACGCATTC GGTCAAGTAT TGGCTAAATA TACTAAATCA GGTAATTTAG ATGCATTTTT | 120  |
| AAATTATAAT AGACAATTGT TCACAAATAT AGACAATATG AACGATTGGT TTATTGATGC | 180  |
| TACAGAAGAC CATGTCTACA TCGCAGAACG CGCTTCTGAG GTCGAAGAAA TTAAAAATTC | 240  |
| TAAACATCGT GCATTCGATA ATTTAAAACG AAGTCACCTT AGAAATACTA TACTCCCACT | 300  |
| ACTGAATATT GATAAAGCAC ATCTTTATTT AATTTCAAAT TATAATGCAA TTGCCTTTGG | 360  |
| TAGTGCAGAG CGATTAGGTA AAAAATCATT AGAAGATATT AAAGATATCG TTAACAAAGC | 420  |
| TGCAGATGGT TATAGAAACT ATTATGATTT CTGGTATCGT CTAGCGTCTG ATAACGTAA  | 480  |
| ACAACGACTA CTAAGAGATG CTGTTATTCC TATTTGGGAA GGTTATAACG CTCCTGGTGG | 540  |
| ATGGGTTGAA AAATATGGCC GCTATAATAC CGACAAAGTA TATACTCCTC TTAGAGAATT | 600  |
| CTTTGGTCCT ATGGATAAGT ATTATAATTA TAATGGAACA GGAGCTTATG CTGCTATATA | 660  |
| TCCTAACTCT GATGATATTA GAACTGATGT AAAATATGTT CATTTAGAAA TGTTTGGTGA | 720  |
| ATACGGTATT TCAGTTTACA CACATGAAAC AACACACGTC AACGACCGTG CGATTTACTT | 780  |
| AGGTGGCTTT GGACACCGTG AAGGTACTGA TGCTGAAGCA TATGCTCAGG GTATGCTACA | 840  |
| AACTCCTGTT ACTGGTAGTG GATTTGATGA GTTTGGTTCT TTAGGTATTA ATATGGTATT | 900  |
| TAAACGCAAA AATGATGGGA ATCAGTGGTA TATTACAGAT CCAAAAACTC TAAAAACACG | 960  |
| AGAAGATATT AATAGATATA TGAAGGGTTA TAATGACACT TTAACCTCTC TTGATGAAAT | 1020 |
| TGAGGCTGAA TCTGTGATTT CTCAACAAAA TAAAGATTTA AATAGTGCAT GGTTCAAAAA | 1080 |
| AATAGATAGA GAATACCGTG ATAACAATAA ATTAAATCAA TGGGATAAAA TTCGAAATCT | 1140 |
| AAGTCAAGAA GAGAAAAATG AATTAAATAT TCAATCTGTT AATGATTTAG TTGATCAACA | 1200 |
| ATTAATGACT AATCGCAATC CAGGTAATGG TATCTATAAA CCCGAAGCAA TTAGCTATAA | 1260 |
| CGATCAATCA CCTTATGTAG GTGTTAGAAT GATGACCGGT ATCTACGGAG GTAATACTAG | 1320 |
| TAAAGGTGCT CCTGGAGCTG TTTCATTCAA ACATAATGCT TTTAGATTAT GGGGTTACTA | 1380 |

CGGATACGAA AATGGGTTCT TAGGTTATGC TTCAAATAAA TATAACAAC AATCTAAAAC 1440  
 AGATGGTGAG TCTGTTCTAA GTGATGAATA TATTATCAAG AAAATATCTA ACAATACATT 1500  
 TAATACTATT GAAGAATTTA AAAAAGCTTA CTTCAAAGAA GTTAAAGATA AAGCAACGAA 1560  
 AGGATTAACA ACATTCGAAG TAAATGGTTC TTCCGTTTCA TCATACGATG ATTTACTGAC 1620  
 ATTGTTTAAA GAAGCTGTTA AAAAAGATGC CGAAACTCTT AAACAAGAAG CAAACGGTAA 1680  
 TAAACAGTA TCTATGAATA ATACAGTTAA ATTAAAAGAA GCTGTTTATA AGAACTTCT 1740  
 TCAACAAACA AATAGCTTTA AAACCTCAAT CTTTAAA 1777

## (2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 592 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Leu Asp Arg Leu Ile Glu Ile Gly Ser Lys Glu Asn Asn Ile Lys Gly  
 1 5 10 15  
 Ser Arg Thr Phe Asp Ala Phe Gly Gln Val Leu Ala Lys Tyr Thr Lys  
 20 25 30  
 Ser Gly Asn Leu Asp Ala Phe Leu Asn Tyr Asn Arg Gln Leu Phe Thr  
 35 40 45  
 Asn Ile Asp Asn Met Asn Asp Trp Phe Ile Asp Ala Thr Glu Asp His  
 50 55 60  
 Val Tyr Ile Ala Glu Arg Ala Ser Glu Val Glu Glu Ile Lys Asn Ser  
 65 70 75 80  
 Lys His Arg Ala Phe Asp Asn Leu Lys Arg Ser His Leu Arg Asn Thr  
 85 90 95  
 Ile Leu Pro Leu Leu Asn Ile Asp Lys Ala His Leu Tyr Leu Ile Ser  
 100 105 110  
 Asn Tyr Asn Ala Ile Ala Phe Gly Ser Ala Glu Arg Leu Gly Lys Lys  
 115 120 125  
 Ser Leu Glu Asp Ile Lys Asp Ile Val Asn Lys Ala Ala Asp Gly Tyr  
 130 135 140  
 Arg Asn Tyr Tyr Asp Phe Trp Tyr Arg Leu Ala Ser Asp Asn Val Lys  
 145 150 155 160  
 Gln Arg Leu Leu Arg Asp Ala Val Ile Pro Ile Trp Glu Gly Tyr Asn  
 165 170 175  
 Ala Pro Gly Gly Trp Val Glu Lys Tyr Gly Arg Tyr Asn Thr Asp Lys  
 180 185 190  
 Val Tyr Thr Pro Leu Arg Glu Phe Phe Gly Pro Met Asp Lys Tyr Tyr

| 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Tyr | Asn | Gly | Thr | Gly | Ala | Tyr | Ala | Ala | Ile | Tyr | Pro | Asn | Ser | Asp |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Ile | Arg | Thr | Asp | Val | Lys | Tyr | Val | His | Leu | Glu | Met | Val | Gly | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Tyr | Gly | Ile | Ser | Val | Tyr | Thr | His | Glu | Thr | Thr | His | Val | Asn | Asp | Arg |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Ile | Tyr | Leu | Gly | Gly | Phe | Gly | His | Arg | Glu | Gly | Thr | Asp | Ala | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Tyr | Ala | Gln | Gly | Met | Leu | Gln | Thr | Pro | Val | Thr | Gly | Ser | Gly | Phe |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Glu | Phe | Gly | Ser | Leu | Gly | Ile | Asn | Met | Val | Phe | Lys | Arg | Lys | Asn |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Gly | Asn | Gln | Trp | Tyr | Ile | Thr | Asp | Pro | Lys | Thr | Leu | Lys | Thr | Arg |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Glu | Asp | Ile | Asn | Arg | Tyr | Met | Lys | Gly | Tyr | Asn | Asp | Thr | Leu | Thr | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Asp | Glu | Ile | Glu | Ala | Glu | Ser | Val | Ile | Ser | Gln | Gln | Asn | Lys | Asp |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Asn | Ser | Ala | Trp | Phe | Lys | Lys | Ile | Asp | Arg | Glu | Tyr | Arg | Asp | Asn |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Asn | Lys | Leu | Asn | Gln | Trp | Asp | Lys | Ile | Arg | Asn | Leu | Ser | Gln | Glu | Glu |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Lys | Asn | Glu | Leu | Asn | Ile | Gln | Ser | Val | Asn | Asp | Leu | Val | Asp | Gln | Gln |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Leu | Met | Thr | Asn | Arg | Asn | Pro | Gly | Asn | Gly | Ile | Tyr | Lys | Pro | Glu | Ala |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ile | Ser | Tyr | Asn | Asp | Gln | Ser | Pro | Tyr | Val | Gly | Val | Arg | Met | Met | Thr |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Gly | Ile | Tyr | Gly | Gly | Asn | Thr | Ser | Lys | Gly | Ala | Pro | Gly | Ala | Val | Ser |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Phe | Lys | His | Asn | Ala | Phe | Arg | Leu | Trp | Gly | Tyr | Tyr | Gly | Tyr | Glu | Asn |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Gly | Phe | Leu | Gly | Tyr | Ala | Ser | Asn | Lys | Tyr | Lys | Gln | Gln | Ser | Lys | Thr |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Asp | Gly | Glu | Ser | Val | Leu | Ser | Asp | Glu | Tyr | Ile | Ile | Lys | Lys | Ile | Ser |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Asn | Asn | Thr | Phe | Asn | Thr | Ile | Glu | Glu | Phe | Lys | Lys | Ala | Tyr | Phe | Lys |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Glu | Val | Lys | Asp | Lys | Ala | Thr | Lys | Gly | Leu | Thr | Thr | Phe | Glu | Val | Asn |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Gly | Ser | Ser | Val | Ser | Ser | Tyr | Asp | Asp | Leu | Leu | Thr | Leu | Phe | Lys | Glu |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |

Ala Val Lys Lys Asp Ala Glu Thr Leu Lys Gln Glu Ala Asn Gly Asn  
 545 550 555 560

Lys Thr Val Ser Met Asn Asn Thr Val Lys Leu Lys Glu Ala Val Tyr  
 565 570 575

Lys Lys Leu Leu Gln Gln Thr Asn Ser Phe Lys Thr Ser Ile Phe Lys  
 580 585 590

## (2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 460 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TAAGACAGAT GAACGGAGCA AGGTGTTTGA CTTTTCATT CCCTACTATA CTGCAAAAAA  | 60  |
| TAAACTCATT GTCAAAAAAT CTGACTTGAC TACTTATCAG TCTGTAAACG ACTTGCGCA  | 120 |
| GAAAAAGGTT GGAGCGCAGA AAGGTCGAT TCAAGAGACG ATGGCGAAAG ATTTGCTACA  | 180 |
| AAATTCTTCC CTCGTATCTC TGCCTAAAAA TGGGAATTTA ATCACAGATT TAAAATCAGG | 240 |
| ACAAGTGGAT GCCGTTATCT TTGAAGAACC TGTTTCCAAG GGATTTGTGG AAAATAATCC | 300 |
| TGATTTAGCA ATCGCAGACC TCAATTTTGA AAAAGAGCAA GATGATTCCT ACGCGGTAGC | 360 |
| CATgAAAAAA GATAGCAAGA AATTGAAGAG GCAGTTCGAT AAAACCATTC AAAAGTTGAA | 420 |
| GGAGTCTGGG GAATTAGACA AACTCATTGA GGAAGCCTTA                       | 460 |

## (2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Lys Thr Asp Glu Arg Ser Lys Val Phe Asp Phe Ser Ile Pro Tyr Tyr  
 1 5 10 15

Thr Ala Lys Asn Lys Leu Ile Val Lys Lys Ser Asp Leu Thr Thr Tyr  
 20 25 30

Gln Ser Val Asn Asp Leu Ala Gln Lys Lys Val Gly Ala Gln Lys Gly  
 35 40 45

Ser Ile Gln Glu Thr Met Ala Lys Asp Leu Leu Gln Asn Ser Ser Leu  
 50 55 60

Val Ser Leu Pro Lys Asn Gly Asn Leu Ile Thr Asp Leu Lys Ser Gly

|                                                                 |     |    |     |    |     |     |
|-----------------------------------------------------------------|-----|----|-----|----|-----|-----|
| 65                                                              |     | 70 |     | 75 |     | 80  |
| Gln Val Asp Ala Val Ile Phe Glu Glu Pro Val Ser Lys Gly Phe Val |     |    |     |    |     |     |
|                                                                 | 85  |    |     | 90 |     | 95  |
| Glu Asn Asn Pro Asp Leu Ala Ile Ala Asp Leu Asn Phe Glu Lys Glu |     |    |     |    |     |     |
|                                                                 | 100 |    | 105 |    |     | 110 |
| Gln Asp Asp Ser Tyr Ala Val Ala Met Lys Lys Asp Ser Lys Lys Leu |     |    |     |    |     |     |
|                                                                 | 115 |    | 120 |    | 125 |     |
| Lys Arg Gln Phe Asp Lys Thr Ile Gln Lys Leu Lys Glu Ser Gly Glu |     |    |     |    |     |     |
|                                                                 | 130 |    | 135 |    | 140 |     |
| Leu Asp Lys Leu Ile Glu Glu Ala Leu                             |     |    |     |    |     |     |
|                                                                 | 145 |    | 150 |    |     |     |

## (2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 751 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CTGTGAGAAT CAAGCTACAC CCAAAGAGAC TAGCGCTCAA AAGACAATCG TCCTTGCTAC | 60  |
| AGCTGGCGAC GTGCCACCAT TTGACTACGA AGACAAGGGC AATCTGACAG GCTTTGATAT | 120 |
| CGAAGTTTTA AAGGCAGTAG ATGAAAAACT CAGCGACTAC GAGATTCAAT TCCAAAGAAC | 180 |
| CGCCTGGGAG AGCATCTTCC CAGGACTTGA TTCTGGTCAC TATCAGGCTG CGGCCAATAA | 240 |
| CTTGAGTTAC ACAAAGAGC GTGCTGAAAA ATACCTTTAC TCGCTTCCAA TTTCCAACAA  | 300 |
| TCCCTCGTC CTTGTCAGCA ACAAGAAAA TCCTTTGACT TCTCTTGACC AGATCGCTGG   | 360 |
| TAAACAACA CAAGAGGATA CCGGAAGTTC TAACGCTCAA TTCATCAATA ACTGGAATCA  | 420 |
| GAAACACACT GATAATCCCG CTACAATTAA TTTTCTGGT GAGGATATTG GTAAACGAAT  | 480 |
| CCTAGACCTT GCTAACGGAG AGTTTGATTT CCTAGTTTTT GACAAGGTAT CCGTTCAAAA | 540 |
| GATTATCAAG GACCGTGGTT TAGACCTCTC AGTCGTTGAT TTACCTTCTG CAGATAGCCC | 600 |
| CAGCAATTAT ATCATTTTCT CAAGCGACCA AAAAGAGTTT AAAGAGCAAT TTGATAAAGC | 660 |
| GCTCAAAGAA CTCTATCAAG ACGGAACCCT TGAAAACTC AGCAATACCT ATCTAGGTGG  | 720 |
| TTCTTACCTC CCAGATCAAT CTCAGTTACA A                                | 751 |

## (2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Glu | Asn | Gln | Ala | Thr | Pro | Lys | Glu | Thr | Ser | Ala | Gln | Lys | Thr | Ile | 1   | 5   | 10  | 15  |
| Val | Leu | Ala | Thr | Ala | Gly | Asp | Val | Pro | Pro | Phe | Asp | Tyr | Glu | Asp | Lys | 20  | 25  | 30  |     |
| Gly | Asn | Leu | Thr | Gly | Phe | Asp | Ile | Glu | Val | Leu | Lys | Ala | Val | Asp | Glu | 35  | 40  | 45  |     |
| Lys | Leu | Ser | Asp | Tyr | Glu | Ile | Gln | Phe | Gln | Arg | Thr | Ala | Trp | Glu | Ser | 50  | 55  | 60  |     |
| Ile | Phe | Pro | Gly | Leu | Asp | Ser | Gly | His | Tyr | Gln | Ala | Ala | Ala | Asn | Asn | 65  | 70  | 75  | 80  |
| Leu | Ser | Tyr | Thr | Lys | Glu | Arg | Ala | Glu | Lys | Tyr | Leu | Tyr | Ser | Leu | Pro | 85  | 90  | 95  |     |
| Ile | Ser | Asn | Asn | Pro | Leu | Val | Leu | Val | Ser | Asn | Lys | Lys | Asn | Pro | Leu | 100 | 105 | 110 |     |
| Thr | Ser | Leu | Asp | Gln | Ile | Ala | Gly | Lys | Thr | Thr | Gln | Glu | Asp | Thr | Gly | 115 | 120 | 125 |     |
| Thr | Ser | Asn | Ala | Gln | Phe | Ile | Asn | Asn | Trp | Asn | Gln | Lys | His | Thr | Asp | 130 | 135 | 140 |     |
| Asn | Pro | Ala | Thr | Ile | Asn | Phe | Ser | Gly | Glu | Asp | Ile | Gly | Lys | Arg | Ile | 145 | 150 | 155 | 160 |
| Leu | Asp | Leu | Ala | Asn | Gly | Glu | Phe | Asp | Phe | Leu | Val | Phe | Asp | Lys | Val | 165 | 170 | 175 |     |
| Ser | Val | Gln | Lys | Ile | Ile | Lys | Asp | Arg | Gly | Leu | Asp | Leu | Ser | Val | Val | 180 | 185 | 190 |     |
| Asp | Leu | Pro | Ser | Ala | Asp | Ser | Pro | Ser | Asn | Tyr | Ile | Ile | Phe | Ser | Ser | 195 | 200 | 205 |     |
| Asp | Gln | Lys | Glu | Phe | Lys | Glu | Gln | Phe | Asp | Lys | Ala | Leu | Lys | Glu | Leu | 210 | 215 | 220 |     |
| Tyr | Gln | Asp | Gly | Thr | Leu | Glu | Lys | Leu | Ser | Asn | Thr | Tyr | Leu | Gly | Gly | 225 | 230 | 235 | 240 |
| Ser | Tyr | Leu | Pro | Asp | Gln | Ser | Gln | Leu | Gln |     |     |     |     |     |     | 245 | 250 |     |     |

## (2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

GACTGGATCC TAAAATCTAC GACAATAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

CTGAGTCGAC TGGTTGTGCT GGTGAG

27

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

GTCAGGATCC AAATTACAAT ACGGACTATG

30

(2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CAGTGTCGAC TAACTCTAGG TCGGAAAC

28

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GACTGGATCC TGAGAATCAA GCTACACCCA AAGAG

35

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

AGTCAAGCTT TTGTAAGTGA GATTGATCTG G

31

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GACTGGATCC TGGTAACCGC TCTTCTCGTA ACGCAGC

37

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

AGTCAAGCTT TTTCAGGAAC TTTTACGCTT CC

32

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

AGTCAGATCT TGTGGAAATT TGACAGGTAA CAGCAAAAAA GCTGC

45

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

ACTGAAGCTT TTTTGT TTTT CAAGAATTCA TCG

33

## (2) INFORMATION FOR SEQ ID NO: 237:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

GACTGGATCC TGGTCAAGGA ACTGCTTCTA AAGAC

35

## (2) INFORMATION FOR SEQ ID NO: 238:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

AGTCAAGCTT TCACAAATTC GTTGGTGAAG CC

32

## (2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

GACTGGATCC TAGCTCAGGT GGAAACGCTG GTTCATCC

38

## (2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

AGTCAAGCTT ATCAACTTTT CCACCTTCAA CAACC

35

## (2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

GTCAAGATCT CTCCAACATAT GGTAATCTG CGGATGG

37

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

AGTCCTGCAG ATCCACATCC GCTTTCATCG GGTAAAGAA GG

42

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

GACTGGATCC TGGGAAAAAT TCTAGCGAAA CTAGTGG

37

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

GTCAGTGCAG CTGTCCTTCT TTTACTTCTT TGGTTGC

37

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

GACTGGATCC TGCTAGCGGA AAAAAAGATA CAACTTCTGG

40

(2) INFORMATION FOR SEQ ID NO: 246:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

CTGAAAGCTT TTTTGCCAAT CCTTCAGCAA TCTTGTC

37

(2) INFORMATION FOR SEQ ID NO: 247:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

GACTAGATCT TGGCTCAAAA AATACAGCTT CAAGTCC

37

(2) INFORMATION FOR SEQ ID NO: 248:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

AGTCCTGCAG GTTTTTGTTT GCTTGGTATT GGTCG

35

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

GACTGGATCC TAGTACAAAC TCAAGCACTA GTCAGACAGA G

41

(2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:  
CAGTCTGCAG TTTCAAAGCT TTTGTATGT CTTC 34
- (2) INFORMATION FOR SEQ ID NO: 251:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:  
GACTGGATCC TGGCAATTCT GCGGAAGTA AAGATGC 37
- (2) INFORMATION FOR SEQ ID NO: 252:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:  
AGTCAAGCTT GTTTCATAGC TTTTGTGATT GTTTCG 36
- (2) INFORMATION FOR SEQ ID NO: 253:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:  
GACTGGATCC TTCACAAGAA AAAACAAAAA ATGAAGATGG 40
- (2) INFORMATION FOR SEQ ID NO: 254:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:  
AGTCAAGCTT ATCGACGTAG TCTCCGCCTT C 31
- (2) INFORMATION FOR SEQ ID NO: 255:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

GACTGGATCC GAAAGGTCTG TGGTCAAATA ATCTTACC

38

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

AGTCAAGCTT AGAGTTAACA TGGTGCTTGC CAATAGG

37

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

GACTGGATCC AAACCTCAGAA AAGAAAGCAG ACAATGC

37

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AGTCAAGCTT CCAAACCTGGT TGATCCAAAC CATCTG

36

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

GACTGGATCC TTCGAAAGGG TCAGAAGGTG CAGACC

36

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

AGTCAAGCTT CTGTAGGCTT GGTGTGCCCC AGTTGC

36

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTGAGGATCC GGGGATGGCA GCTTTTAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 262:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CAGTAAGCTT GTTTACCCAT TCACCATTAC C

31

(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CAGTGGATCC AGACGAGCAA AAAATTAAG

29

(2) INFORMATION FOR SEQ ID NO: 264:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

TCAGAAGCTT GTTTACCCAT TCACCATT

28

(2) INFORMATION FOR SEQ ID NO: 265:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

GACTGGATCC CTGTGGTGAG GAAGAACTA AAAAG

35

(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

CTGAGTCGAC AATATTCTGT AGGAATGCTT CGAATTTG

38

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

CTGAGGATCC GACTTTTAAC AATAAACTA TTGAAGAG

38

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

GTCAGTGCAG GTTGTCACCT CCAAAAATCA CGG

33

## (2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GACTGGATCC CTTTACAGGT AAACAACTAC AAGTCGG

37

## (2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

CAGTAAGCTT TTCGAAGTTT GGCTCAGAAT TG

32

## (2) INFORMATION FOR SEQ ID NO: 271:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

GACTGGATCC CCAGGCTGAT ACAAGTATCG CA

32

## (2) INFORMATION FOR SEQ ID NO: 272:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CAGTAAGCTT ATCTGCAGTA TGGCTAGATG G

31

## (2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:  
GACTGGATCC GTCTGTATCA TTTGAAAACA AAGAAAC 37  
(2) INFORMATION FOR SEQ ID NO: 274:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:  
CAGTCTGCAG TTTTACTGTT GCTGTGCTTG TG 32  
(2) INFORMATION FOR SEQ ID NO: 275:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:  
ACTGAGATCT TGGTCAAAAG GAAAGTCAGA CAGGAAAGG 39  
(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:  
CAGTAAGCTT ATTCTGAGC TTTTTTGATA AAGGTTGCGC A 41  
(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:  
ACTGGGATCC GAAGGATAGA TATATTTTAG CATTTGAGAC 40  
(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

AGTCAAGCTT CCATGGTATC AAAGGCAAGA CTTGG

35

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

GTCAGGATCC GGTAGTTAAA GTTGGTATTA ACGG

34

(2) INFORMATION FOR SEQ ID NO: 280:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

AGTCAAGCTT GCAATTTTTG CGAAGTATTC CAAGAG

36

(2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

AGTCGGATCC TTCTTACGAG TTGGGACTGT ATCAAGC

37

(2) INFORMATION FOR SEQ ID NO: 282:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:  
AGTCAAGCTT GTTTATTTTT TCCTTACTTA CAGATGAAGG 40

(2) INFORMATION FOR SEQ ID NO: 283:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:  
AGTCGGATCC TACTGAGATG CATCATAATC TAGGAGC 37

(2) INFORMATION FOR SEQ ID NO: 284:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:  
TCAGCTCGAG TTCTTTGACA TCTCCATCAT AAGTCGC 37

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:  
GACTGGATCC GGTTTTGAGA AAGTATTTGC AGGGG 35

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:  
CAGTAAGCTT GGATTTTTTC ATGGATGCAA TTTTTTTGG 39

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GACTGGATCC GACAACATTT ACTATCCATA CAGTAGAGTC AGC

43

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

GACTAAGCTT GGCATAAGGT TGCAATTCTG GATTAATTGG

40

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

GACTGGATCC GGCTAAGGAA AGAGTGGATG

30

(2) INFORMATION FOR SEQ ID NO: 290:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GACTAAGCTT TTCATTTTTA AATTGACTAT GCGCCCG

37

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

GACTGGATCC TTGTTCTAT GAACTTGGTC GTCACC

36

(2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CATGAAGCTT ATCCTGGATT TTTCCAAGTA AATCT

35

(2) INFORMATION FOR SEQ ID NO: 293:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

GACTGGATCC TTATAAGGGT GAATTAGAAA AAGG

34

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

GACTAAGCTT CTTATTAGGA TTGTTAGTAG TTG

33

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

GACTGGATCC GAATGTTTCAG GCTCAAGAAA GTTCAGG

37

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GACTAAGCTT TTCCCCTGAT GGAGCAAAGT AATACC

36

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

GACTGGATCC CTTGGGTGTA ACCCATATCC AGCTCCTTCC

40

(2) INFORMATION FOR SEQ ID NO: 298:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

GACTGTCGAC TTCAGCTTGT TTATCTGGGG TTGC

34

(2) INFORMATION FOR SEQ ID NO: 299:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

GACTGGATCC TAGTGATGGT ACTTGGCAAG GAAAACAG

38

(2) INFORMATION FOR SEQ ID NO: 300:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

ACTGCTGCAG ATCTTTGCCA CCTAGCTTCT CATTG

35

## (2) INFORMATION FOR SEQ ID NO: 301:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

GTCAGGATCC TGGGATTCAA TATGTCAGAG ATGATACTAG

40

## (2) INFORMATION FOR SEQ ID NO: 302:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

CTAGAAGCTT ACGCACCCAT TCACCATTAT CATTG

35

## (2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

GTCAGGATCC GGATAATAGA GAAGCATTA AACC

35

## (2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AGTCAAGCTT GACAAAATCT TGAAACTCCT CTGGTC

36

## (2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

GTCAGGATCC AGATTTTGTC GAGGAGTGTC ATACC

35

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

AGTCAAGCTT TCCCTTTTTC CCCTTACGAA TCCAGG

36

(2) INFORMATION FOR SEQ ID NO: 307:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GACTGGATCC ATCTGTAGTT TATGCGGATG AAACACTTAT TAC

43

(2) INFORMATION FOR SEQ ID NO: 308:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

GACTGTCGAC GCTTTGGTAG AGATAGAAGT CATG

34

(2) INFORMATION FOR SEQ ID NO: 309:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

GACTGGATCC TTACTTTGGT ATCGTAGATA CAGCCGGC

38

(2) INFORMATION FOR SEQ ID NO: 310:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

AGTCAAGCTT TGTTAATTGC GTACCTTCTA AGCGACC

37

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

GACTGGATCC AGCTAAGGTT GCATGGGATG CGATTCTG

37

(2) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

GACTGTCGAC CTGGGCTTTA TTAGTTTGAC TAGC

34

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

CAGTGGATCC CTATCACTAT GTAAATAAAG AGA

33

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:  
ACTGAAGCTT TTCTGTCCCT GTTTGAGGCA 30
- (2) INFORMATION FOR SEQ ID NO: 315:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:  
CAGTGGATCC TGAGACTCCT CAATCAATAA CAAA 34
- (2) INFORMATION FOR SEQ ID NO: 316:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:  
ACGTAAGCTT ATAATCAGTA GGAGAACTG AACT 34
- (2) INFORMATION FOR SEQ ID NO: 317:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:  
CAGTGGATCC GGATGCTCAA GAACTGCGG 30
- (2) INFORMATION FOR SEQ ID NO: 318:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:  
GACTAAGCTT TTGCCTCTCA TTCTTGCTTC C 31
- (2) INFORMATION FOR SEQ ID NO: 319:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

CAGTGGATCC CGACAAAGGT GAGACTGAG

29

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

ACGTAAGCTT ATTTCTTAAT TCAAGTGTTC TCTCTG

36

(2) INFORMATION FOR SEQ ID NO: 321:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GACTGGATCC AAATCAATTG GTAGCACAAG ATCC

34

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CAGTGTGAC ATTAGGAGCC ACTGGTCTC

29

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

CAGTGGATCC CAAACAGTCA GCTTCAGGAA C

31

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

GACTCTGCAG TTTAATCTTG TCCCAGGTGG

30

(2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

GACTGGATCC ATTCGATGAT GCGGATGAAA AG

32

(2) INFORMATION FOR SEQ ID NO: 326:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

GACTAAGCTT CATTTGTCTT TGGGTATTTTC GCA

33

(2) INFORMATION FOR SEQ ID NO: 327:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

CAGTGGATCC GGAGAGTCGA TCAAAAGTAG

30

(2) INFORMATION FOR SEQ ID NO: 328:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

GTCACTGCAG TTGCTCGTCT CGAGGTTC

28

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

CAGTGGATCC ATGGACAACA GGAAACTGGG AC

32

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

CAGTAAGCTT ATTAGCTTCT GTACCTGTGT TTG

33

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

GACTGGATCC CGATGGGCTC AATCCAACCC CAGGTCAAGT C

41

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GACTCTGCAG CATAGCTTTA TCCTCTGACA TCATCGTATC

40

## (2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

GACTGGATCC TTCCAATCAA AAACAGGCAG ATGG

34

## (2) INFORMATION FOR SEQ ID NO: 334:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

GACTAAGCTT GAGTCCCATA GTCCAAGGCA

30

## (2) INFORMATION FOR SEQ ID NO: 335:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

AGTCGGATCC TATCACAGGA TCGAACGGTA AGACAACC

38

## (2) INFORMATION FOR SEQ ID NO: 336:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

ACTGGTCGAC TTCTTTTAAC TCCGCTACTG TGTC

34

## (2) INFORMATION FOR SEQ ID NO: 337:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:  
CAGTGGATCC AAGTTCATCG AAGATGGTTG GGAAGTCC 38

(2) INFORMATION FOR SEQ ID NO: 338:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:  
GATCGTCGAC CCGCTCCAC ATGCTCAACC TT 32

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:  
TGACGGATCC ATCGCTAGCT AGTGAAATGC AAGAAAG 37

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:  
TGACAAGCTT ATTCGTTTTT GAACTAGTTG CTTTCGT 37

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:  
GACTGGATCC GCACCAGATG GGGCACAAGG TTCAGGG 37

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

TGACAAGCTT AACTTGTAAC GAACAGTTCA ATCTG

35

(2) INFORMATION FOR SEQ ID NO: 343:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

GACTAGATCT TTTTAACCCA ACTGTTGGTA CTTTCC

36

(2) INFORMATION FOR SEQ ID NO: 344:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TGACAAGCTT GTTAGGTGTT ACATTTTGAC CGTC

34

(2) INFORMATION FOR SEQ ID NO: 345:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

ACTGAGATCT TTTTAACCCA ACTGTTGGTA CTTTC

35

(2) INFORMATION FOR SEQ ID NO: 346:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

GACTAAGCTT TCTACGATAA CGATCATTTT CTTTACC

37

(2) INFORMATION FOR SEQ ID NO: 347:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

GACTGTGCGAC TCGTAGATAT TTAAGTCTAA GTGAAGCG

38

(2) INFORMATION FOR SEQ ID NO: 348:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

AGTCAAGCTT GTTAGGTGTT ACATTTTGCA AGTC

34

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GACTGGATCC CTTTGGTTTT GAAGGAAGTA AG

32

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

TGACCTGCAG ACGATTTTTG AAAAATGGAG GTGTATC

37

(2) INFORMATION FOR SEQ ID NO: 351:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

CAGTGGATCC CTACTACCTC TCGAGAGAAA G

31

(2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

ACTGAAGCTT TTCGCTTTTT ACTCGTTTGA CA

32

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CAGTGGATCC TAAGGTCAAA AGTCAGACCG CTAAGAAAGT GC

42

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

CAGTAAGCTT TAGGGTATCC AAATACTGGT TGTGATG

38

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

TGACAGATCT TGACGGGTCT CAGGATCAGA CTCAGG

36

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

TGACAAGCTT CAAAGACATC CACCTCTTGA CCTTTG

36

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

GACTGGATCC TAGAGGCTTT GCCAAATGGT GGGAAGGG

38

(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

GTCAGTCGAC TTGTTGTAAC ACTTTTCGAG GTTTGGTACC

40

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CAGTGGATCC TCAAAAAGAG AAGGAAACT TGG

33

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CAGTCTGCAG TTTCTTCAAC AAACCTTGTT CTTG

34

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

CAGTGGATCC ACGTTCTATT GAGGACCACT T

31

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

CAGTAAGCTT TTCCTTCTCA GTCAATTCTT TTCC

34

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GACTGGATCC CGCTCAAAAT ACCAGAGGTG TTCAG

35

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

GACTAAGCTT AGTACCATGG GTGTGACAGG TTTGAA

36

## (2) INFORMATION FOR SEQ ID NO: 365:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

CTGAGGATCC AATTGTACAA TTAGAAAAAG ATAGC

35

## (2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

TGACAAGCTT GCGTTGACTA GGTTCTGCAA TGCC

34

## (2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

GACTGGATCC TCTGACCAAG CAAAAGAAG CAGTCAATGA

40

## (2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

TCAGCAGCTG ATCATTGACT TTACGATTG CTCC

34

## (2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:  
 GACTGGATCC GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC G 41

(2) INFORMATION FOR SEQ ID NO: 370:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:  
 TCAGAAGCTT ATTTTTTGTT TCCTTAATGC GTT 33

(2) INFORMATION FOR SEQ ID NO: 371:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:  
 GACTGGATCC GGGACAAATT CAAAAAATA GGCAAGAGG 39

(2) INFORMATION FOR SEQ ID NO: 372:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:  
 GTCAAAGCTT TGGCTCTTTG ATTGCCAACA ACTG 34

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:  
 GACTGGATCC TCGCTACCAG CAACAAAGCG AGCAAAAGG 39

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

GACTAAGCTT ACTTTTTTCT TTTTCCACAC GA

32

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

CAGTGGATCC GAACCGACAA GTCGCCCACT ATCAAGACT

39

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CTGAAAGCTT TGAATTCTCT TTCTTTTCAG GCT

33

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

TCGAGGATCC GGTGTGCGGC TGGCAATATA TCCCGT

36

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CAGTAAGCTT CCGAACCCAT TCGCCATTAT AGTTGAC

37

(2) INFORMATION FOR SEQ ID NO: 379:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

AGTCGGATCC GGCCAAATCA GAATGGGTAG AAGAC

35

(2) INFORMATION FOR SEQ ID NO: 380:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

TGACCTGCAG CTTCTCATTG ATTTTCATCA TCAC

34

(2) INFORMATION FOR SEQ ID NO: 381:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACTGGATCC ATTTGCAGAT GATTCTGAAG GATGG

35

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

TCAGCTGCAG CTTAACCCAT TCACCATTCT AGTTTAAG

38

(2) INFORMATION FOR SEQ ID NO: 383:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

GACTGGATCC TGTCGCTGCA AATGAACTG AAGTAGC

37

(2) INFORMATION FOR SEQ ID NO: 384:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

GACTAAGCTT ATACCAAACG CTGACATCTA CGCG

34

(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

AGTCAGATCT TACGTCTCAG CCTACTTTTG TAAGAGC

37

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

GACTAAGCTT AACCCATTCA CCATTGGCAT TGAC

34

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

CAGTGGATCC TGGACAGGTG AAAGGTCATG CTACATTTGT G

41

(2) INFORMATION FOR SEQ ID NO: 388:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

GACTAAGCTT CAACCATTTGA GACCTTGCAA CAC

33

(2) INFORMATION FOR SEQ ID NO: 389:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

GTCAGGATCC GATTGCTCCT TTGAAGGATT TGAGAGAAAC C

41

(2) INFORMATION FOR SEQ ID NO: 390:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GACTAAGCTT CGATCAAAGA TAAGATAAAT ATATATAAAG T

41

(2) INFORMATION FOR SEQ ID NO: 391:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GACTGGATCC TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGG

47

(2) INFORMATION FOR SEQ ID NO: 392:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

TGACAAGCTT ATCTATCAGC TCATTTAATC GTTTTTG

37

(2) INFORMATION FOR SEQ ID NO: 393:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CTGAGGATCC CAACGTTGAG AATTATTTGC GAATG

35

(2) INFORMATION FOR SEQ ID NO: 394:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

TGACAAGCTT GAGTCTACAA AAGTAATGTA C

31

(2) INFORMATION FOR SEQ ID NO: 395:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

GTCAGGATCC CTACTATCAA TCAAGTTCTT CAGCC

35

(2) INFORMATION FOR SEQ ID NO: 396:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

TGACAAGCTT GACTGAGGCT TGGACCAGAT TGAAAAG

37

## (2) INFORMATION FOR SEQ ID NO: 397:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

GACTGGATCC GACAAAAACA TTAAACGTC CTGAGG

36

## (2) INFORMATION FOR SEQ ID NO: 398:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

GACTAAGCTT AGCACGAACT GTGACGCTGG TTCC

34

## (2) INFORMATION FOR SEQ ID NO: 399:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

GACTGGATCC TTCTCAGGAG ACCTTTAAAA ATATC

35

## (2) INFORMATION FOR SEQ ID NO: 400:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

GACTAAGCTT GTTGGCCATC TTGTACATAC C

31

## (2) INFORMATION FOR SEQ ID NO: 401:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:  
GACTGGATCC AGTAAATGCG CAATCAAATT C 31
- (2) INFORMATION FOR SEQ ID NO: 402:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:  
AGTCCTGCAG GTATTTAGCC CAATAATCTA TAAAGCT 37
- (2) INFORMATION FOR SEQ ID NO: 403:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:  
CAGTGGATCC TTACCGCGTT CATCAAGATG TC 32
- (2) INFORMATION FOR SEQ ID NO: 404:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:  
GACTAAGCTT GCCAGATGTT GAAAAGAGAG TG 32
- (2) INFORMATION FOR SEQ ID NO: 405:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:  
GACTGGATCC GTGGATGGGC TTAACTATC TTCGTATTCG 40
- (2) INFORMATION FOR SEQ ID NO: 406:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

AGTCAAGCTT GCTAGTCTTC ACTTTCCCTT TCC

33

(2) INFORMATION FOR SEQ ID NO: 407:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

GACTGTCGAC ACTAAACCAG CATCGTTCGC AGGA

34

(2) INFORMATION FOR SEQ ID NO: 408:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

CTGACTGCAG CTTCTTGAAG AAATAATGAT TGTGG

35

(2) INFORMATION FOR SEQ ID NO: 409:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

CAGTGGATCC TGACTACCTT GAAATCCCAC TT

32

(2) INFORMATION FOR SEQ ID NO: 410:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:  
CAGTAAGCTT TTTTSTAAGG TTGTAGAATG ATTTCAATC 39
- (2) INFORMATION FOR SEQ ID NO: 411:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:  
CAGTGTGCGAC TCGTATCTTT TTTTGGAGCA ATGTT 35
- (2) INFORMATION FOR SEQ ID NO: 412:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:  
GACTAAGCTT AAATGTTCCG ATACGGGTGA TTG 33
- (2) INFORMATION FOR SEQ ID NO: 413:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:  
CAGTGGATCC GGACTCTCTC AAAGATGTGA AAG 33
- (2) INFORMATION FOR SEQ ID NO: 414:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:  
GACTAAGCTT CTTGAGTTTG TCAAGGATTG CTTT 34
- (2) INFORMATION FOR SEQ ID NO: 415:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

CAGTGGATCC CAAGAAATCC TATCATCTCT TCCAGAAG

38

(2) INFORMATION FOR SEQ ID NO: 416:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

GACTAAGCTT TTCAGAACTA AAAGCCGCAG CTT

33

(2) INFORMATION FOR SEQ ID NO: 417:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

GACTGGATCC ACGAAATGCA GGGCAGACAG

30

(2) INFORMATION FOR SEQ ID NO: 418:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

CAGTAAGCTT ATCAACATAA TCTAGTAAAT AAGCGT

36

(2) INFORMATION FOR SEQ ID NO: 419:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

CAGTGGATCC TGTATAGTTT TTAGCGCTTG TTCTTC

36

(2) INFORMATION FOR SEQ ID NO: 420:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

GTCAAAGCTT TGATAGAGTG TCATAATCTT CTTTAG

36

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

GACTGGATCC GTGTGTCGAG CATATTCTGA AG

32

(2) INFORMATION FOR SEQ ID NO: 422:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

CAGTAAGCTT ACTTTTACCA TTTCTTTGTT CTGCATC

37

(2) INFORMATION FOR SEQ ID NO: 423:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

GACTGTCGAC GTGTTTGGAT AGCATTCAGA ATCAGACG

38

(2) INFORMATION FOR SEQ ID NO: 424:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

CAGTAAGCTT CGGAAGTAAA GACAATTTTT CC

32

(2) INFORMATION FOR SEQ ID NO: 425:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

CAGTGGATCC GTGCCTAGAT AGTATTATTA CTCAAAC

37

(2) INFORMATION FOR SEQ ID NO: 426:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

GACTAAGCTT TTTGCTTATT TCTCTCAATT TTTC

34

(2) INFORMATION FOR SEQ ID NO: 427:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

CAGTGGATCC CATTCAGAAG CAGACCTATC AAAATC

36

(2) INFORMATION FOR SEQ ID NO: 428:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

ACTGAAGCTT ATGTAATTTT TTAGATTTTT CAATATTTTT CAG

43

## (2) INFORMATION FOR SEQ ID NO: 429:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AGTCGGATCC TAAGGCTGAT AATCGTGTTT AAATG

35

## (2) INFORMATION FOR SEQ ID NO: 430:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

GACTAAGCTT AAAATTAGAT AGACGTTGAG T

31

## (2) INFORMATION FOR SEQ ID NO: 431:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

AGTCGGATCC CTGTGGCAAT CAGTCAGCTG CTTCC

35

## (2) INFORMATION FOR SEQ ID NO: 432:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

GACTGTCGAC TTTAATCTTG TCCCAGGTGG TTAATTTGCC

40

## (2) INFORMATION FOR SEQ ID NO: 433:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

ACTGGTCGAC TTGTCAACAA CAACATGCTA CTTCTGAG

38

(2) INFORMATION FOR SEQ ID NO: 434:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

GACTCTGCAG AAGTTTAACC CACTTATCAT TATCC

35

(2) INFORMATION FOR SEQ ID NO: 435:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

ACTGGGATCC TTGTTTCAGGC AAGTCCGTGA CTAGTGAAC

39

(2) INFORMATION FOR SEQ ID NO: 436:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

GACTAAGCTT GGCTAATTCC TTCAAAGTTT GCA

33

(2) INFORMATION FOR SEQ ID NO: 437:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

AGTCGGATCC CTCGCAAATT GAAAAGGCGG CAGTTAGCC

39

(2) INFORMATION FOR SEQ ID NO: 438:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

GACTAAGCTT GTAAATAAGC GTACCTTTTT CTTC

35

(2) INFORMATION FOR SEQ ID NO: 439:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

TCAGGGATCC TTGTCAGTCA GGTCTAATG GTTCTCAG

38

(2) INFORMATION FOR SEQ ID NO: 440:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

AGTCAAGCTT GGCATTGGCG TCGCCGTCCT TC

32

(2) INFORMATION FOR SEQ ID NO: 441:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

GACTGGATCC GGAAACTTCA CAGGATTTTA AAGAGAAG

38

(2) INFORMATION FOR SEQ ID NO: 442:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:  
GACTGTCGAC AATCAATCCT TCTTCTGCAC TTCT 34
- (2) INFORMATION FOR SEQ ID NO: 443:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:  
CAGTGGATCC TGTGCTCGAA GTTGAGACTC CTCAATC 37
- (2) INFORMATION FOR SEQ ID NO: 444:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:  
GACTAAGCTT TTCTTCAAAT TTATTATCAG C 31
- (2) INFORMATION FOR SEQ ID NO: 445:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:  
AGTCGGATCC AACACCTGTA TATAAAGTTA CAGCAATCG 39
- (2) INFORMATION FOR SEQ ID NO: 446:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:  
GACTGTCGAC TACTTGACCG AATGCGTCGA ATGTACG 37
- (2) INFORMATION FOR SEQ ID NO: 447:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

CTGAGGATCC ATTAGACAGA TTAATTGAAA TCGG

34

(2) INFORMATION FOR SEQ ID NO: 448:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

GACTGTGCGAC TTAAAGATT GAAGTTTAA AGCT

34

(2) INFORMATION FOR SEQ ID NO: 449:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

TGACGGATCC TAAGACAGAT GAACGGAGCA AGGTG

35

(2) INFORMATION FOR SEQ ID NO: 450:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

CTGAAAGCTT TAAGGCTTCC TCAATGAGTT TGTCT

35

(2) INFORMATION FOR SEQ ID NO: 451:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

GACTGGATCC CTGTGAGAAT CAAGCTACAC CCA

33

(2) INFORMATION FOR SEQ ID NO: 452:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

CTGAAAGCTT TTGTAAGTGA GATTGATCTG GGAG

34

(2) INFORMATION FOR SEQ ID NO:453:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Leu Ala Ser Gly Ala Cys  
1 5

(2) INFORMATION FOR SEQ ID NO:454:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Leu Pro Xaa Thr Gly Xaa  
1 5